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PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Docket No: 01017/35136

CONTINUING APPLICATION TRANSMITTAL UNDER 37 CFR 1.53(b)

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

This is a request under 37 CFR 1.53 for filing a

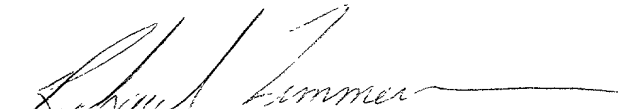
- ☐ continuation application.
☒ divisional application.

1. Particulars of Prior Application

Application Serial No: 09/005,893
Filed on: January 12, 1998
Title: Stem Cell Factor
Art Unit: 1801
Examiner: Draper, G.
Prior Docket No.: 01017/34463

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Continuing Application Transmittal Under 37 CFR 1.53(b) and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **December 31, 1998**, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. **EM 362 726 034 US**.


Richard Zimmermann

2. This request is filed by:

1. Full Name of Inventor	Family Name Zsebo	First Given Name Kriszkina	Second Given Name M.
Residence & Citizenship	City Thousand Oaks	State or Foreign Country: California	Country of Citizenship USA
Post Office Address	Post Office Address 1043 Mountain Oak Place	City Oakland	State & Zip Code/Country California 91300

2. Full Name of Inventor	Family Name Bosselman	First Given Name Robert	Second Given Name A.
Residence & Citizenship	City Thousand Oaks	State or Foreign Country: California	Country of Citizenship USA
Post Office Address	Post Office Address 3301 Baccarat	City Thousand Oaks	State & Zip Code/Country California 91362

3. Full Name of Inventor	Family Name Suggs	First Given Name Sidney	Second Given Name V.
Residence & Citizenship	City Newbury Park	State or Foreign Country: California	Country of Citizenship USA
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4. Full Name of Inventor	Family Name Martin	First Given Name Francis	Second Given Name H.
Residence & Citizenship	City Thousand Oaks	State or Foreign Country: California	Country of Citizenship USA
Post Office Address	Post Office Address 337 North Green Meadow Avenue	City Thousand Oaks	State & Zip Code/Country California 91320

☐ This application is being filed by less than all the inventors named in the prior application. An accompanying statement requests deletion of the name(s) of the person(s) who are not inventors of the invention being claimed in this application.

3. Amendments

- ☐ Amend the specification by inserting before the first line the sentence:
--This is a of U.S. application Serial No. , filed --
- ☐ Cancel claims in the prior application before calculating the filing fee.
- ☒ A Preliminary Amendment is enclosed.
- ☒ The filing fee is based upon entry of the foregoing amendment(s) (if any).

4. Copy of Prior Application

- ☒ The enclosed is a copy of the prior complete application, including the specification (with claims), drawings, the oath or declaration, and any amendments referred to in the oath or declaration filed to complete the prior application.

5. Incorporation By Reference

The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under paragraph 4, above, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. Priority

- ☐ Priority of application No. _____, filed on _____ in _____ is claimed under 35 USC 119.
- ☐ The certified copy(ies) was(were) filed in prior U.S. application Serial No. _____.
- ☐ The certified copy(ies) has(have) not been filed.

7. Assignment

- ☒ The prior application is assigned of record to AMGEN INC., and has been recorded at Reel No. 5440, Frame No. 0012.

8. Small Entity Status

- ☐ Verified statement(s) claiming small entity status is(are) attached.
- ☐ Small entity status has been established in the prior application and is still proper and desired.

9. Fee Calculation

CLAIMS AS FILED - INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$380.00		\$760.00
TOTAL	70-20	= 50	X 9 =	\$	X 18 =	\$900.00
INDEP.	1-3	= 0	X 39 =	\$	X 78 =	\$0.00
<input checked="" type="checkbox"/> First Presentation of Multiple Dependent Claim			+ 130 =	\$	+ 260 =	\$260.00
Filing Fee:				\$	OR	\$1,920.00

10. Method of Payment of Fees

- ☒ Attached is a check in the amount of: \$ 1,920.00
- ☐ Charge Deposit Account No. 13-2855 in the amount of: \$ _____

11. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge any fees which may be required during the pendency of this application under 37 CFR 1.16 or 37 CFR 1.17 to Deposit Account No. 13-2855. A copy of this Transmittal is enclosed.

Please refund any overpayment to Marshall, O'Toole, Gerstein, Murray & Borun at the address below.

Respectfully submitted,

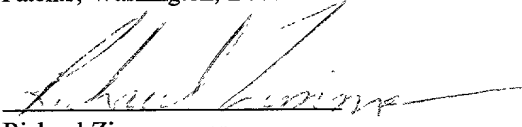
MARSHALL, O'TOOLE, GERSTEIN,
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By: _____

David W. Clough
Reg. No: 36,107

December 31, 1998

IN THE UNITED STATES PATENT
AND TRADEMARK OFFICE

Applicant: Zsebo et al.)	"Express Mail" mailing label No. EM 362 726 034 US.
)	
Serial No.: Unknown)	Date of Deposit: December 31, 1998
)	
Filed: Unknown)	I hereby certify that this paper (or fee) is being
)	deposited with the United States Postal Service
)	"EXPRESS MAIL POST OFFICE TO ADDRESSEE"
For: STEM CELL FACTOR:)	service under 37 CFR §1.110 on the date indicated
COMPOSITION CLAIMS)	above and is addressed to: Assistant Commissioner for
)	Patents, Washington, D.C. 20231
)	
Group Art Unit: Unknown)	
)	
Examiner: Unknown)	Richard Zimmermann

PRELIMINARY AMENDMENT, SEQUENCE LISTING
and STATEMENT UNDER 37 CFR §1.821(f)

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

Prior to examination please amend application as follows:

IN THE SPECIFICATION:

Please amend the specification as follows:

Please delete first paragraph on page 1 (lines 3-10) and replace therefore with:

--This is a divisional application of Serial No. 09/005,893, filed January 12, 1998, which is a divisional application of Serial No. 08/ 449,653, filed May 24, 1995, which is a divisional of Serial No. 08/172,329, filed December 21, 1993, which is a continuation of 07/982,255, filed November 25, 1992, which is a continuation of Serial No. which is a continuation-in-part of Serial No. 07/589,701, filed October 1, 1990, which is a continuation-in-part application of Ser. No. 07/ 573,616 filed August 24, 1990, which is a continuation-in-

part application of Ser. No. 07/ 537,198 filed June 11, 1990, which is a continuation-in-part application of Ser. No. 07/ 422,383 filed October 16, 1989, all of which are hereby incorporated by reference.--

Please replace pages 187-197 with pages 187-259 attached herewith.

Page 9, line 10 after "sequence" insert --(SEQ. ID NO.: 1)--.

Page 9, line 14 after "cDNA" insert --(SEQ ID NOS.: 2-19)--.

Page 9, line 15 after "DNA" insert --(SEQ ID NOS.: 20-30)--.

Page 9, line 16 after "oligonucleotides" insert --(SEQ ID NOS.: 31-38)--.

Page 9, line 26 after "rat" insert --(SEQ ID NOS.: 39 and 40)--.

Page 9, line 29 after "protein" insert --(SEQ ID NOS.: 41 and 42)--.

Page 9, line 34 after "human" insert --(SEQ ID NOS.: 43 and 44)--.

Page 10, line 1 after "of" insert --(SEQ ID NOS.: 45 and 46)--.

Page 10, line 4 after "including" insert --(SEQ ID NOS.: 47 and 48)--.

Page 10, line 8 after "rat" insert --(SEQ ID NOS.: 49-57)--.

Page 10, line 16 after "from" insert --(SEQ ID NOS.: 58 and 59)--.

Page 13, line 26 after "sequence" insert --(SEQ ID NOS.: 60 and 61)--.

Page 13, line 33 after "sequence" insert --(SEQ ID NOS.: 62 and 63)--.

Page 49, line 32 after "..." insert --(SEQ ID NO.: 64)--.

Page 51, line 7 after "(M)" insert --(SEQ ID NO.: 65)--.

Page 51, line 9 after "K----" insert --(SEQ ID NO.: 66)--.

Page 51, line 11 after "(M)" insert --(SEQ ID NO.: 67)--.

Page 51, line 15 after "A-----" insert --(SEQ ID NO.: 68)--.

Page 52, line 17 after "R" insert --(SEQ ID NO.: 69)--.

Page 52, line 18 after "-K" insert --(SEQ ID NO.: 70)--.

Page 52, line 19 after "-K" insert --(SEQ ID NO.: 71)--.

Page 52, line 20 after "-R" insert --(SEQ ID NO.: 72)--.

Page 52, line 22 after "L-R" insert --(SEQ ID NO.: 73)--.

Page 52, line 24 after "G----" insert --(SEQ ID NO.: 74)--.

Page 52, line 26 after "-R" insert --(SEQ ID NO.: 75)--.

Page 52, line 28 after "-R" insert --(SEQ ID NO.: 76)--.
 Page 53, line 16 after "E" insert --(SEQ ID NO.: 77)--.
 Page 53, line 17 after "(A)" insert --(SEQ ID NO.: 78)--.
 Page 53, line 21 after "S-D" insert --(SEQ ID NO.: 79)--.
 Page 53, line 24 after "T-S-D" insert --(SEQ ID NO.: 80)--.
 Page 54, line 20 after "Asp----" insert --(SEQ ID NO.: 81)--.
 Page 55, line 29 after "(A)" --insert --(SEQ ID NO.: 82)--.
 Page 55, line 31 after "(A)" insert --(SEQ ID NO.: 83)--.
 Page 64, line 23 after "224-24" insert --(SEQ ID NO.: 10)--.
 Page 64, line 24 after "-3')" insert --(SEQ ID NO.: 84)--.
 Page 64, line 26 after "-3')" insert --(SEQ ID NO.: 85)--.
 Page 64, line 27 after "-3')" insert --(SEQ ID NO.: 86)--.
 Page 75, line 28 after "-3)" insert --(SEQ ID NO.: 87)--.
 Page 80, line 29 after "283-19" insert --(SEQ ID NO.: 85)--.
 Page 80, line 29 after "283-20" insert --(SEQ ID NO.: 86)--.
 Page 80, line 31 after "-3')" insert --(SEQ ID NO.: 88)--.
 Page 80, line 33 after "227-29" insert --(SEQ ID NO.: 14)--.
 Page 80, line 33 after "-3'" insert --(SEQ ID NO.: 89)--.
 Page 80, line 34 after "-3')" insert --(SEQ ID NO.: 90)--.
 Page 84, line 36 after "3'" insert --(SEQ ID NO.: 91)--.
 Page 84, line 37 after "5'" insert --(SEQ ID NO.: 92)--.
 Page 87, line 7 after "3'" insert --(SEQ ID NO.: 93)--.
 Page 90, line 8 after "(Ala)" insert --(SEQ ID NO.: 94)--.
 Page 90, line 19 after "-Ala" insert --(SEQ ID NO.: 95)--.
 Page 91, line 20 after "3'" insert --(SEQ ID NO.: 96)--.
 Page 91, line 21 after "5'" insert --(SEQ ID NO.: 97)--.
 Page 92, line 7 after "TATGCAGGA" insert --(SEQ ID NO.: 98)--.
 Page 92, line 8 after "ACGTCCTCTAG" insert --(SEQ ID NO.: 99)--.
 Page 93, line 23 after "TATGGAAGGTATCTGCA" insert --(SEQ ID NO.: 100)--.
 Page 93, line 24 after "ACCTTCCATAG" insert --(SEQ ID NO.: 101)--.
 Page 145, line 24 after "tttccttATG" insert --(SEQ ID NO.: 102)--.

Page 145, line 25 after "gccgccgccATG" insert --(SEQ ID NO.: 103)--.

Page 145, line 26 after "3'" insert --(SEQ ID NO.: 104)--.

IN THE CLAIMS:

Cancel claims 1-70 without prejudice to Applicants' right to further prosecute claims of the same or similar scope in duly filed continuation, continuation-in-part and/or divisional applications.

Enter claims 71-114 as follows:

--71. A composition which comprises a therapeutically effective amount of stem cell factor (SCF) polypeptide or biologically active fragment or analog thereof and one or more cytokines in a pharmaceutically acceptable carrier.

72. The composition of claim 71, wherein SCF polypeptide is a product of a recombinant prokaryote cell or eukaryote cells.

73. The composition of claim 72, wherein the SCF polypeptide is a human SCF polypeptide.

74. The composition of claim 73, wherein the SCF polypeptide is selected from the group of polypeptides consisting of the amino acid sequence set out as 1-162, 1-164 and 1-165 as set out in Figure 15C, said polypeptides optionally consisting of an N-terminal methionine.

75. The composition of claim 73, wherein the SCF polypeptide is selected from the group of polypeptides consisting of the amino acid sequence set out as 1-100, 1-110, 1-120, 1-123, 1-127, 1-130, 1-133, 1-137, 1-141, 1-145, 1-148, 1-152, 1-156, 1-157, 1-158, 1-159, 1-160, 1-161, 1-163, 1-166, 1-168, 1-173, 1-178, 2-164, 2-165, 5-164, 11-

164, 1-180, 1-183, 1-185, 1-188, 1-189, 1-220 and 1-248 as set out in Figures 42A-C, said polypeptide optionally consisting of an N-terminal methionine.

76. The composition of claim 73, wherein the SCF polypeptide is selected from the group consisting of amino acids 1-152, 1-157, 1-160, 1-161 and 1-220 as set out in Figures 44A-C, said polypeptide optionally consisting of N-terminal methionine.

77. The method of claims 74, 75, or 76, wherein the stem cell factor is covalently conjugated to a water-soluble polymer.

78. The method of claim 77, wherein the water soluble polymer is polyethylene glycol.

79. The composition of claim 74, 75, or 76, wherein the amount of SCF in the composition is effective to treat hematopoietic disorders.

80. The composition of claim 77, wherein the amount of SCF in the composition is effective to treat hematopoietic disorders.

81. The composition of claim 74, 75, or 76, wherein the amount of SCF in the composition is effective to treat epithelial cell disorders.

82. The composition of claim 77 wherein the amount of SCF in the composition is effective to treat epithelial cell disorders.

83. The composition of claim 74, 75, or 76, wherein the amount of SCF in the composition is effective to treat stromal cell disorders.

84. The composition of claim 77, wherein the amount of SCF in the composition is effective to treat stromal cell disorders.

85. The composition of claim 74, 75, or 76, wherein the amount of SCF in the composition is effective to treat neural disorders.

86. The composition of claim 77, wherein the amount of SCF in the composition is effective to treat neural disorders.

87. The composition of claim 74, 75, or 76, wherein the amount of SCF in the composition is effective to treat pigmentation disorders.

88. The composition of claim 77, wherein the amount of SCF in the composition is effective to treat pigmentation disorders.

89. The composition of claim 74, 75, or 76, wherein the amount of SCF in the composition is effective to treat germ cell disorders.

90. The composition of claim 77, wherein the amount of SCF in the composition is effective to treat germ cell disorders.

91. The composition of claim 79, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

92. The composition of claim 80, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

93. The composition of claim 81, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

94. The composition of claim 82, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

95. The composition of claim 83, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

96. The composition of claim 84, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

97. The composition of claim 85, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

98. The composition of claim 86, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

99. The composition of claim 87, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

100. The composition of claim 88, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

101. The composition of claim 89, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

102. The composition of claim 90, wherein the composition contains at least one cytokine selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, EPO, G-CSF, GM-CSF, CSF-1, IGF-1, and LIF.

103. The composition of claim 74, 75, or 76, wherein the composition contains a pharmaceutically effective carrier for the controlled release of SCF and other cytokines in the composition.

104. The composition of claim 77, wherein the composition contains a pharmaceutically effective carrier for the controlled release of SCF and other cytokines in the composition

105. The composition of claim 74, 75, or 76, wherein the composition contains a pharmaceutically effective carrier for parenteral delivery of the composition.

106. The composition of claim 77, wherein the composition contains a pharmaceutically effective carrier for parenteral delivery of the composition.

107. The composition of claim 74, 75, or 76, wherein the composition contains a pharmaceutically effective carrier for pulmonary delivery of the composition.

108. The composition of claim 77, wherein the composition contains a pharmaceutically effective carrier for pulmonary delivery of the composition.

109. The composition of claim 74, 75, or 76, wherein the composition contains a pharmaceutically effective carrier for nasal delivery of the composition.

110. The composition of claim 77, wherein the composition contains a pharmaceutically effective carrier for nasal delivery of the composition.

111. The composition of claim 74, 75, or 76, wherein the composition contains a pharmaceutically effective carrier for the oral delivery of the composition.

112. The composition of claim 77, wherein the composition contains a pharmaceutically effective carrier for the oral delivery of the composition.

113. The composition of claim 74, 75, or 76, wherein the composition contains a pharmaceutically effective carrier for the topical delivery of the composition.

114. The composition of claim 77, wherein the composition contains a pharmaceutically effective carrier for the topical delivery of the composition.--

PRELIMINARY REMARKS

I. Amendment to the Specification

Amendment to the specification is made to bring the disclosure of particular nucleic acid and amino acid sequences, and the Sequence Listing itself in line with 37 C.F.R. §1.821(c). A computer readable form of the Sequence Listing in accordance with 37 C.F.R. §1.821(e) is concurrently submitted herewith. The content of the paper copy and computer readable forms are the same as required under 37 C.F.R. §1.821(f). The addition of the Sequence Listing necessitates renumbering subsequent pages in the application. Renumbering of the pages in the claims and abstract is requested to maintain clarity in the order of the application and adds no new matter to the application.

If the Examiner believes that submission of a substitute specification incorporating the above-requested amendments would materially facilitate handling by the Patent Office, telephone advice of the same to the undersigned would be appreciated.

II. Amendment to the Claims

Support for the claims 71-114 is found throughout the specification. Specifically, support for the recombinant SCF and SCF fragments recited in claims 71-76 is found in canceled claim 39, Fig. 15C, 42A-D, 44A-C and also found variously on page 182, beginning on line 30 (1-100, 1-110, 1-120, 1-123, 1-127, 1-130, and 1-133), page

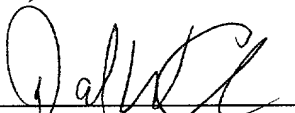
182, beginning on line 10 (1-137, 1-141, 1-145, 1-148, 1-156, 1-157, 1-158, 1-159, 1-160, 1-161, 1-162, 1-163, 1-166, 1-168, 1-173, and 1-178), page 93, line 11 (1-164), page 183 beginning on line 7 (2-164, 5-164, and 11-164), page 183 beginning on line 34 (1-180, 1-185, 1-188, and 1-189), page 184 beginning on line 7 (1-152 and 1-157), page 93, line 12 (1-183) page 184 beginning on line 9 (1-165 and 2-165) and on page 184, line 2 (1-220). Support for the recited SCF fragments in claim 73 is found on page 185, lines 12-13.

Support for compositions of SCF polypeptides of claims 71 -114 is found throughout the application. Support for pharmaceutical compositions containing is specifically found on page 24, line 26 through page 26, line 5. Support for modified and/or conjugated SCF polypeptides such as pegylated SCF is found in Example 13, page 135, line 6 through page 138, line 8. Use of SCF polypeptides in combination with other cytokines is discussed throughout the application especially on page 27, line 1 through line 7; in Example 21, page 156, line 9 through page 160, line 33; in Example 22, page 161, line 1 through page 164, line 7; in Example 24, page 168, line 18 through page 170, line 27; in Example 25, page 170, line 29 through page 175, line 35; and in Example 26, page 176, line 1 through page 179, line 28. Support for the production and characterization of SCF analogs and fragments is found in Example 28, page 182-185.

Respectfully submitted,

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By


David W. Clough
(Reg. No. 36,107)

Chicago, Illinois
December 31, 1998

STEM CELL FACTOR

This is a continuation-in-part application of Serial No. 589,701, filed October 1, 1990 which is a
5 continuation-in-part application of Ser. No. 573,616
filed August 24, 1990 which is a continuation-in-part
application of Ser. No. 537,198 filed June 11, 1990
which is a continuation-in-part application of Ser. No.
422,383 filed October 16, 1989 hereby incorporated by
10 reference.

The present invention relates in general to novel factors which stimulate primitive progenitor cells including early hematopoietic progenitor cells, and to
DNA sequences encoding such factors. In particular, the
15 invention relates to these novel factors, to fragments and polypeptide analogs thereof and to DNA sequences encoding the same.

Background of the Invention

20 The human blood-forming (hematopoietic) system is comprised of a variety of white blood cells (including neutrophils, macrophages, basophils, mast cells, eosinophils, T and B cells), red blood cells
25 (erythrocytes) and clot-forming cells (megakaryocytes, platelets),

It is believed that small amounts of certain hematopoietic growth factors account for the differentiation of a small number of "stem cells" into a
30 variety of blood cell progenitors for the tremendous proliferation of those cells, and for the ultimate differentiation of mature blood cells from those lines. The hematopoietic regenerative system functions well under normal conditions. However, when stressed by
35 chemotherapy, radiation, or natural myelodysplastic disorders, a resulting period during which patients are

seriously leukopenic, anemic, or thrombocytopenic occurs. The development and the use of hematopoietic growth factors accelerates bone marrow regeneration during this dangerous phase.

5 In certain viral induced disorders, such as acquired autoimmune deficiency (AIDS) blood elements such as T cells may be specifically destroyed. Augmentation of T cell production may be therapeutic in such cases.

10 Because the hematopoietic growth factors are present in extremely small amounts, the detection and identification of these factors has relied upon an array of assays which as yet only distinguish among the different factors on the basis of stimulative effects on
15 cultured cells under artificial conditions.

 The application of recombinant genetic techniques has clarified the understanding of the biological activities of individual growth factors. For example, the amino acid and DNA sequences for human
20 erythropoietin (EPO), which stimulates the production of erythrocytes, have been obtained. (See, Lin, U. S. Patent 4,703,008, hereby incorporated by reference). Recombinant methods have also been applied to the isolation of cDNA for a human granulocyte colony-
25 stimulating factor, G-CSF (See, Souza, U. S. Patent 4,810,643, hereby incorporated by reference), and human granulocyte-macrophage colony stimulating factor (GM-CSF) [Lee, et al., Proc. Natl. Acad. Sci. USA, 82, 4360-4364 (1985); Wong, et al., Science, 228, 810-814
30 (1985)], murine G- and GM-CSF [Yokota, et al., Proc. Natl. Acad. Sci. (USA), 81, 1070 (1984); Fung, et al., Nature, 307, 233 (1984); Gough, et al., Nature, 309, 763 (1984)], and human macrophage colony-stimulating factor (CSF-1) [Kawasaki, et al., Science, 230, 291 (1985)].

35 The High Proliferative Potential Colony Forming Cell (HPP-CFC) assay system tests for the action

of factors on early hematopoietic progenitors [Zont, J. Exp. Med., 159, 679-690 (1984)]. A number of reports exist in the literature for factors which are active in the HPP-CFC assay. The sources of these factors are indicated in Table 1. The most well characterized factors are discussed below.

An activity in human spleen conditioned medium has been termed synergistic factor (SF). Several human tissues and human and mouse cell lines produce an SF, referred to as SF-1, which synergizes with CSF-1 to stimulate the earliest HPP-CFC. SF-1 has been reported in media conditioned by human spleen cells, human placental cells, 5637 cells (a bladder carcinoma cell line), and EMT-6 cells (a mouse mammary carcinoma cell line). The identity of SF-1 has yet to be determined. Initial reports demonstrate overlapping activities of interleukin-1 with SF-1 from cell line 5637 [Zsebo et al., Blood, 71, 962-968 (1988)]. However, additional reports have demonstrated that the combination of interleukin-1 (IL-1) plus CSF-1 cannot stimulate the same colony formation as can be obtained with CSF-1 plus partially purified preparations of 5637 conditioned media [McNiece, Blood, 73, 919 (1989)].

The synergistic factor present in pregnant mouse uterus extract is CSF-1. WEHI-3 cells (murine myelomonocytic leukemia cell line) produce a synergistic factor which appears to be identical to IL-3. Both CSF-1 and IL-3 stimulate hematopoietic progenitors which are more mature than the target of SF-1.

Another class of synergistic factor has been shown to be present in conditioned media from TC-1 cells (bone marrow-derived stromal cells). This cell line produces a factor which stimulates both early myeloid and lymphoid cell types. It has been termed hemolymphopoietic growth factor 1 (HLGF-1). It has an apparent molecular weight of 120,000 [McNiece et al., Exp. Hematol., 16, 383 (1988)].

Of the known interleukins and CSFs, IL-1, IL-3, and CSF-1 have been identified as possessing activity in the HPP-CFC assay. The other sources of synergistic activity mentioned in Table 1 have not been structurally identified. Based on the polypeptide sequence and biological activity profile, the present invention relates to a molecule which is distinct from IL-1, IL-3, CSF-1 and SF-1.

10

Table 1
Preparations Containing Factors Active
in the HPP-CFC Assay

15	Source ¹	Reference
	Human Spleen CM	[Kriegler, <u>Blood</u> , <u>50</u> , 503(1982)]
	Mouse Spleen CM	[Bradley, <u>Exp. Hematol. Today</u> Baum, ed., 285 (1980)]
20	Rat Spleen CM	[Bradley, supra, (1980)]
	Mouse lung CM	[Bradley, supra, (1980)]
	Human Placental CM	[Kriegler, supra (1982)]
	Pregnant Mouse Uterus	[Bradley, supra (1980)]
	GTC-C CM	[Bradley, supra (1980)]
25	RH3 CM	[Bradley, supra (1980)]
	PHA PBL	[Bradley, supra (1980)]
	WEHI-3B CM	[McNiece, <u>Cell Biol. Int. Rep.</u> , <u>6</u> , 243(1982)]
	EMT-6 CM	[McNiece, <u>Exp. Hematol.</u> , <u>15</u> , 854 (1987)]
	L- Cell CM	[Kriegler, <u>Exp. Hematol.</u> , <u>12</u> , 844 (1984)]
30	5637 CM	[Stanley, <u>Cell</u> , <u>45</u> , 667 (1986)]
	TC-1 CM	[Song, <u>Blood</u> , <u>66</u> , 273 (1985)]

¹ CM= Conditioned media.

35

When administered parenterally, proteins are often cleared rapidly from the circulation and may

therefore elicit relatively short-lived pharmacological activity. Consequently, frequent injections of relatively large doses of bioactive proteins may be required to sustain therapeutic efficacy. Proteins modified by the covalent attachment of water-soluble polymers such as polyethylene glycol, copolymers of polyethylene glycol and polypropylene glycol, carboxymethyl cellulose, dextran, polyvinyl alcohol, polyvinylpyrrolidone or polyproline are known to exhibit substantially longer half-lives in blood following intravenous injection than do the corresponding unmodified proteins [Abuchowski et al., In: "Enzymes as Drugs", Holcenberg et al., eds. Wiley-Interscience, New York, NY, 367-383 (1981), Newmark et al., J. Appl. Biochem. 4:185-189 (1982), and Katre et al., Proc. Natl. Acad. Sci. USA 84, 1487-1491 (1987)]. Such modifications may also increase the protein's solubility in aqueous solution, eliminate aggregation, enhance the physical and chemical stability of the protein, and greatly reduce the immunogenicity and antigenicity of the protein. As a result, the desired in vivo biological activity may be achieved by the administration of such polymer-protein adducts less frequently or in lower doses than with the unmodified protein.

Attachment of polyethylene glycol (PEG) to proteins is particularly useful because PEG has very low toxicity in mammals [Carpenter et al., Toxicol. Appl. Pharmacol., 18, 35-40 (1971)]. For example, a PEG adduct of adenosine deaminase was approved in the United States for use in humans for the treatment of severe combined immunodeficiency syndrome. A second advantage afforded by the conjugation of PEG is that of effectively reducing the immunogenicity and antigenicity of heterologous proteins. For example, a PEG adduct of a human protein might be useful for the treatment of disease in other mammalian species without the risk of triggering a severe immune response.

Polymers such as PEG may be conveniently attached to one or more reactive amino acid residues in a protein such as the alpha-amino group of the amino-terminal amino acid, the epsilon amino groups of lysine side chains, the sulfhydryl groups of cysteine side chains, the carboxyl groups of aspartyl and glutamyl side chains, the alpha-carboxyl group of the carboxyl-terminal amino acid, tyrosine side chains, or to activated derivatives of glycosyl chains attached to certain asparagine, serine or threonine residues.

Numerous activated forms of PEG suitable for direct reaction with proteins have been described. Useful PEG reagents for reaction with protein amino groups include active esters of carboxylic acid or carbonate derivatives, particularly those in which the leaving groups are N-hydroxysuccinimide, p-nitrophenol, imidazole or 1-hydroxy-2-nitrobenzene-4-sulfonate. PEG derivatives containing maleimido or haloacetyl groups are useful reagents for the modification of protein free sulfhydryl groups. Likewise, PEG reagents containing amino, hydrazine or hydrazide groups are useful for reaction with aldehydes generated by periodate oxidation of carbohydrate groups in proteins.

It is an object of the present invention to provide a factor causing growth of early hematopoietic progenitor cells.

Summary of the Invention

According to the present invention, novel factors, referred to herein as "stem cell factors" (SCF) having the ability to stimulate growth of primitive progenitors including early hematopoietic progenitor cells are provided. These SCFs also are able to stimulate non-hematopoietic stem cells such as neural stem cells and primordial germ stem cells. Such factors

include purified naturally-occurring stem cell factors. The invention also relates to non-naturally-occurring polypeptides having amino acid sequences sufficiently duplicative of that of naturally-occurring stem cell factor to allow possession of a hematopoietic biological activity of naturally occurring stem cell factor.

The present invention also provides isolated DNA sequences for use in securing expression in procaryotic or eukaryotic host cells of polypeptide products having amino acid sequences sufficiently duplicative of that of naturally-occurring stem cell factor to allow possession of a hematopoietic biological activity of naturally occurring stem cell factor. Such DNA sequences include:

- (a) DNA sequences set out in Figures 14B, 14C, 15B, 15C, 15D, 42 and 44 or their complementary strands;
- (b) DNA sequences which hybridize to the DNA sequences defined in (a) or fragments thereof; and
- (c) DNA sequences which, but for the degeneracy of the genetic code, would hybridize to the DNA sequences defined in (a) and (b).

Also provided are vectors containing such DNA sequences, and host cells transformed or transfected with such vectors. Also comprehended by the invention are methods of producing SCF by recombinant techniques, and methods of treating disorders. Additionally, pharmaceutical compositions including SCF and antibodies specifically binding SCF are provided.

The invention also relates to a process for the efficient recovery of stem cell factor from a material containing SCF, the process comprising the steps of ion exchange chromatographic separation and/or reverse phase liquid chromatographic separation.

The present invention also provides a biologically-active adduct having prolonged in vivo half-

life and enhanced potency in mammals, comprising SCF covalently conjugated to a water-soluble polymer such as polyethylene glycol or copolymers of polyethylene glycol and polypropylene glycol, wherein said polymer is
5 unsubstituted or substituted at one end with an alkyl group. Another aspect of this invention resides in a process for preparing the adduct described above, comprising reacting the SCF with a water-soluble polymer having at least one terminal reactive group and purifying
10 the resulting adduct to produce a product with extended circulating half-life and enhanced biological activity.

Brief Description of the Drawings

15 Figure 1 is an anion exchange chromatogram from the purification of mammalian SCF.

Figure 2 is a gel filtration chromatogram from the purification of mammalian SCF.
20

Figure 3 is a wheat germ agglutinin-agarose chromatogram from the purification of mammalian SCF.

Figure 4 is a cation exchange chromatogram
25 from the purification of mammalian SCF.

Figure 5 is a C_4 chromatogram from the purification of mammalian SCF.

30 Figure 6 shows sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis (PAGE) (SDS-PAGE) of C_4 column fractions from Figure 5.

35 Figure 7 is an analytical C_4 chromatogram of mammalian SCF.

Figure 8 shows SDS-PAGE of C₄ column fractions from Figure 7.

Figure 9 shows SDS-PAGE of purified mammalian SCF and deglycosylated mammalian SCF.

Figure 10 is an analytical C₄ chromatogram of purified mammalian SCF.

Figure 11 shows the amino acid sequence of mammalian SCF derived from protein sequencing.

Figure 12 shows

- A. oligonucleotides for rat SCF cDNA
- B. oligonucleotides for human SCF DNA
- C. universal oligonucleotides.

Figure 13 shows

- A. a scheme for polymerase chain reaction (PCR) amplification of rat SCF cDNA
- B. a scheme for PCR amplification of human SCF cDNA.

Figure 14 shows

- A. sequencing strategy for rat genomic DNA
- B. the nucleic acid sequence of rat genomic DNA.
- C. the nucleic acid sequence of rat SCF cDNA and amino acid sequence of rat SCF protein.

Figure 15 shows

- A. the strategy for sequencing human genomic DNA
- B. the nucleic acid sequence of human genomic DNA

C. the composite nucleic acid sequence of human SCF cDNA and amino acid sequence of SCF protein.

D. the nucleic acid sequence of genomic DNA and amino acid sequence of human SCF protein, including flanking regions and introns.

Figure 16A and B shows the aligned amino acid sequences of human, monkey, dog, mouse, and rat SCF protein.

Figure 16C shows an elution profile of hSCF¹⁻²⁴⁸ from CHO cells after AspN peptidase digestion and HPLC.

Figure 16D shows the nucleotide sequence of the 221 base pair EcoRI-BamHI fragment constructed from oligonucleotides that were used in creating the plasmid for human [Met⁻¹] SCF¹⁻¹⁶⁵. Uppercase letters below the nucleotide sequence represent the amino acid sequence.

Lowercase letters above the nucleotide sequence show nucleotides in the original hSCF¹⁻¹⁸³ sequence that were altered to generate codons most frequently used by E. coli.

Figure 16E shows the 39 base pair BstEII-BamHI fragment used in creating the plasmid for human [Met⁻¹] SCF¹⁻¹⁶⁵ with optimized C-terminal codons.

Figure 17 shows the structure of mammalian cell expression vector V19.8 SCF.

Figure 18 shows the structure of mammalian CHO cell expression vector pDSVE.1.

Figure 19 shows the structure of E. coli expression vector pCFM1156.

Figure 20 shows

A. a radioimmunoassay of mammalian SCF

B. SDS-PAGE of immune-precipitated
mammalian SCF.

5

Figure 21 shows Western analysis of
recombinant human SCF.

Figure 22 shows Western analysis of
10 recombinant rat SCF.

Figure 22A shows radioimmune assay
determination of SCF in Human Serum. The percent
inhibition of ^{125}I -human SCF binding produced was
15 determined for various doses of an unlabeled standard of
CHO HuSCF¹⁻²⁴⁸ (solid circles); a sample of NHS Lot
500080713 (open circles); and NHS Lot 500081015 (solid
triangle).

20 Figure 23 is a bar graph showing the effect of
COS-1 cell-produced recombinant rat SCF on bone marrow
transplantation.

Figure 24 shows the effect of recombinant rat
25 SCF on curing the macrocytic anemia of Steel mice.

Figure 25 shows the peripheral white blood
cell count (WBC) of Steel mice treated with recombinant
rat SCF.

30

Figure 26 shows the platelet counts of Steel
mice treated with recombinant rat SCF.

Figure 27 shows the differential WBC count for
35 Steel mice treated with recombinant rat SCF¹⁻¹⁶⁴ PEG25.

Figure 28 shows the lymphocyte subsets for Steel mice treated with recombinant rat SCF¹⁻¹⁶⁴ PEG25.

Figure 29 shows the effect of recombinant human sequence SCF treatment of normal primates in increasing peripheral WBC count.

Figure 30 shows the effect of recombinant human sequence SCF treatment of normal primates in increasing hematocrits and platelet numbers.

Figure 31 shows photographs of

A. human bone marrow colonies stimulated by recombinant human SCF¹⁻¹⁶²

B. Wright-Giemsa stained cells from colonies in Figure 31 A.

Figure 31C shows proliferation of the UT-7 cell line by E. coli derived SCFs. Open squares are human [Met⁻¹]SCF¹⁻¹⁶⁴, crosses and open diamonds are human [Met⁻¹]SCF¹⁻¹⁶⁵.

Figure 32 shows SDS-PAGE of S-Sepharose column fractions from chromatogram shown in Figure 33

A. with reducing agent
B. without reducing agent.

Figure 33 is a chromatogram of an S-Sepharose column of E. coli derived recombinant human SCF.

Figure 34 shows SDS-PAGE of C₄ column fractions from chromatogram showing Figure 35

A. with reducing agent
B. without reducing agent.

Figure 35 is a chromatogram of a C₄ column of E. coli derived recombinant human SCF.

Figure 36 is a chromatogram of a Q-Sepharose column of CHO derived recombinant rat SCF.

Figure 37 is a chromatogram of a C₄ column of CHO derived recombinant rat SCF.

Figure 38 shows SDS-PAGE of C₄ column fractions from chromatogram shown in Figure 37.

Figure 39 shows SDS-PAGE of purified CHO derived recombinant rat SCF before and after de-glycosylation.

Figure 40 shows

- A. gel filtration chromatography of recombinant rat pegylated SCF¹⁻¹⁶⁴ reaction mixture
- B. gel filtration chromatography of recombinant rat SCF¹⁻¹⁶⁴, unmodified.

Figure 41 shows labelled SCF binding to fresh leukemic blasts.

Figure 42 shows human SCF cDNA sequence obtained from the HT1080 fibrosarcoma cell line.

Figure 43 shows an autoradiograph from COS-7 cells expressing human SCF¹⁻²⁴⁸ and CHO cells expressing human SCF¹⁻¹⁶⁴.

Figure 44 shows human SCF cDNA sequence obtained from the 5637 bladder carcinoma cell line.

Figure 45 shows the enhanced survival of irradiated mice after SCF treatment.

Figure 46 shows the enhanced survival of irradiated mice after bone marrow transplantation with 5% of a femur and SCF treatment.

Figure 47 shows the enhanced survival of irradiated mice after bone marrow transplantation with 0.1 and 20% of a femur and SCF treatment.

Figure 48 shows radioprotection effects of rat SCF on survival of mice after irradiation.

Figure 49 shows radioprotection effects of rat SCF on survival of mice after irradiation.

Figure 50 shows a single coinjection of rrSCF plus G-CSF causes an increase in circulating neutrophils that is approximately additive as compared to the rrSCF alone- and G-CSF alone-induced neutrophilia. The kinetics of rrSCF plus G-CSF-induced neutrophilia reflect the combined effect of the differing kinetics of rrSCF-induced neutrophilia peaking at 6 hours and G-CSF-induced neutrophilia peaking at 12 hours.

Figure 51 shows daily coinjection of rrSCF and G-CSF for one week caused a highly synergistic increase in circulating neutrophils with a marked linear increase between day 4 and day 6.

Figure 52 shows a kinetic study of rrSCF plus G-CSF-induced neutrophilia after the seventh daily injection shows that the peak of circulating neutrophils occurs at 12 hours and reaches a level of 69×10^3 PMN/mm³.

Figure 53 shows in vivo administration of SCF-platelet counts.

Figure 54 shows dose response of rratSCF-PEG on platelet counts.

Figure 55 shows effect of 5-FU on platelet levels.

Figure 56 shows 5-FU effect on ACH+ cells in marrow.

Figure 57 shows mean platelet volume after 5-FU treatment.

Figure 58 shows SCF mRNA levels after 5-FU treatment. The data in this figure were generated from the same marrow samples collected in Figure 56. Data points are the values determined from individual mice.

Figure 59 shows the effects of HuSCF and zidovudine on peripheral blood BFU-E in normal donors. Light density cells were plated in duplicate in the presence of (A) 1 U/ml or (B) 4 U/ml of erythropoietin, four concentrations of zidovudine (0, 10^{-7} M, 10^{-6} M and 10^{-5} M) and four concentrations of HuSCF (0, 10 ng/ml, 100 ng/ml and 1000 ng/ml). The bars represent the mean \pm S.E.M. for the duplicate determinations of both normal donors. All of the increases for HuSCF are statistically significant (independent t-test, 2-tailed, $p < 0.01$).

Figure 60 shows the effects of HuSCF and zidovudine on peripheral blood BFU-E in normal and HIV-infected donors. Light density cells were plated in duplicate in the presence of 1 U/ml of erythropoietin

and four concentrations of HuSCF (0, 10 ng/ml, 100 ng/ml and 1000 ng/ml). The bars represent the mean for the duplicate determinations.

5 Figure 61 shows alteration of the BFU-E ID₅₀ of zidovudine by HuSCF. The 50% inhibitory concentration for BFU-E for each level of HuSCF was calculated as described in the text. The bars represent the mean for the two normal donors.

10 Figure 62 shows effects of HuSCF on AZT suppression of bone marrow culture as measured by BFU-E.

15 Figure 63 shows effect of HuSCF on AZT suppression of bone marrow culture as measured by CFU-GM.

20 Figure 64 shows effects of HuSCF on gancyclovir suppression of bone marrow culture as measured by BFU-E.

25 Figure 65 shows effect of HuSCF on gancyclovir suppression of bone marrow culture as measured by CFU-GM.

 Figure 66 shows effect of rat SCF alone and in combination with CFU-S number in a pre-CFU-S assay.

30 Figure 67 shows effect of SCF alone and in combination on the recovery of hemaglobin.

35 Figure 68 shows fluorescence emission spectra of human SCF¹⁻¹⁶⁴. Emission intensity is shown for CHO cell derived [Met⁻¹]SCF¹⁻¹⁶² (dotted line) and E. coli derived [Met⁻¹]SCF¹⁻¹⁶⁴ (solid line).

Figure 69 shows circular dichroism of SCF. The far ultraviolet spectra (A) and near ultraviolet spectra (B) are shown for CHO cell-derived [Met⁻¹]SCF¹⁻¹⁶² (dotted line) and E. coli derived
5 [Met⁻¹]SCF¹⁻¹⁶⁴ (solid line).

Figure 70 shows second derivative infrared spectra of SCF. The second derivative infrared spectra in the amide I region (1700-1620 cm⁻¹) for E. coli
10 derived [Met⁻¹]SCF¹⁻¹⁶⁴ (A) and CHO cell derived [Met⁻¹]SCF¹⁻¹⁶² (B) are shown.

Numerous aspects and advantages of the invention will be apparent to those skilled in the art
15 upon consideration of the following detailed description which provides illustrations of the practice of the invention in its presently-preferred embodiments.

Detailed Description of the Invention

20 According to the present invention, novel stem cell factors and DNA sequences coding for all or part of such SCFs are provided. The term "stem cell factor" or "SCF" as used herein refers to naturally-occurring SCF
25 (e.g. natural human SCF) as well as non-naturally occurring (i.e., different from naturally occurring) polypeptides having amino acid sequences and glycosylation sufficiently duplicative of that of naturally-occurring stem cell factor to allow possession
30 of a hematopoietic biological activity of naturally-occurring stem cell factor. Stem cell factor has the ability to stimulate growth of early hematopoietic progenitors which are capable of maturing to erythroid, megakaryocyte, granulocyte, lymphocyte, and macrophage
35 cells. SCF treatment of mammals results in absolute increases in hematopoietic cells of both myeloid and

lymphoid lineages. One of the hallmark characteristics of stem cells is their ability to differentiate into both myeloid and lymphoid cells [Weissman, Science, 241, 58-62 (1988)]. Treatment of Steel mice (Example 8B)

5 with recombinant rat SCF results in increases of granulocytes, monocytes, erythrocytes, lymphocytes, and platelets. Treatment of normal primates with recombinant human SCF results in increases in myeloid and lymphoid cells (Example 8C).

10 There is embryonic expression of SCF by cells in the migratory pathway and homing sites of melanoblasts, germ cells, hematopoietic cells, brain and spinal chord.

15 Early hematopoietic progenitor cells are enriched in bone marrow from mammals which has been treated with 5-Fluorouracil (5-FU). The chemotherapeutic drug 5-FU selectively depletes late hematopoietic progenitors. SCF is active on post 5-FU bone marrow.

20 The biological activity and pattern of tissue distribution of SCF demonstrates its central role in embryogenesis and hematopoiesis as well as its capacity for treatment of various stem cell deficiencies.

25 The present invention provides DNA sequences which include: the incorporation of codons "preferred" for expression by selected nonmammalian hosts; the provision of sites for cleavage by restriction endonuclease enzymes; and the provision of additional initial, terminal or intermediate DNA sequences which
30 facilitate construction of readily-expressed vectors. The present invention also provides DNA sequences coding for polypeptide analogs or derivatives of SCF which differ from naturally-occurring forms in terms of the identity or location of one or more amino acid residues
35 (i.e., deletion analogs containing less than all of the residues specified for SCF; substitution analogs, wherein

one or more residues specified are replaced by other residues; and addition analogs wherein one or more amino acid residues is added to a terminal or medial portion of the polypeptide) and which share some or all the
5 properties of naturally-occurring forms. The present invention specifically provides DNA sequences encoding the full length unprocessed amino acid sequence as well as DNA sequences encoding the processed form of SCF.

Novel DNA sequences of the invention include
10 sequences useful in securing expression in procaryotic or eucaryotic host cells of polypeptide products having at least a part of the primary structural conformation and one or more of the biological properties of naturally-occurring SCF. DNA sequences of the invention
15 specifically comprise: (a) DNA sequences set forth in Figures 14B, 14C, 15B, 15C, 15D, 42 and 44 or their complementary strands; (b) DNA sequences which hybridize (under hybridization conditions disclosed in Example 3 or more stringent conditions) to the DNA sequences in
20 Figures 14B, 14C, 15B, 15C, 15D, 42, and 44 or to fragments thereof; and (c) DNA sequences which, but for the degeneracy of the genetic code, would hybridize to the DNA sequences in Figures 14B, 14C, 15B, 15C, 15D, 42, and 44. Specifically comprehended in parts (b) and
25 (c) are genomic DNA sequences encoding allelic variant forms of SCF and/or encoding SCF from other mammalian species, and manufactured DNA sequences encoding SCF, fragments of SCF, and analogs of SCF. The DNA sequences may incorporate codons facilitating transcription and
30 translation of messenger RNA in microbial hosts. Such manufactured sequences may readily be constructed according to the methods of Alton et al., PCT published application WO 83/04053.

According to another aspect of the present
35 invention, the DNA sequences described herein which encode polypeptides having SCF activity are valuable for

the information which they provide concerning the amino acid sequence of the mammalian protein which have heretofore been unavailable. The DNA sequences are also valuable as products useful in effecting the large scale
5 synthesis of SCF by a variety of recombinant techniques. Put another way, DNA sequences provided by the invention are useful in generating new and useful viral and circular plasmid DNA vectors, new and useful transformed and transfected procaryotic and eucaryotic
10 host cells (including bacterial and yeast cells and mammalian cells grown in culture), and new and useful methods for cultured growth of such host cells capable of expression of SCF and its related products.

DNA sequences of the invention are also
15 suitable materials for use as labeled probes in isolating human genomic DNA encoding SCF and other genes for related proteins as well as cDNA and genomic DNA sequences of other mammalian species. DNA sequences may also be useful in various alternative methods of protein
20 synthesis (e.g., in insect cells) or in genetic therapy in humans and other mammals. DNA sequences of the invention are expected to be useful in developing transgenic mammalian species which may serve as eucaryotic "hosts" for production of SCF and SCF
25 products in quantity. See, generally, Palmiter et al., Science 222, 809-814 (1983).

The present invention provides purified and isolated naturally-occurring SCF (i.e. purified from nature or manufactured such that the primary, secondary
30 and tertiary conformation, and the glycosylation pattern are identical to naturally-occurring material) as well as non-naturally occurring polypeptides having a primary structural conformation (i.e., continuous sequence of amino acid residues) and glycosylation sufficiently
35 duplicative of that of naturally occurring stem cell factor to allow possession of a hematopoietic biological

activity of naturally occurring SCF. Such polypeptides include derivatives and analogs.

In a preferred embodiment, SCF is characterized by being the product of procaryotic or eucaryotic host expression (e.g., by bacterial, yeast, higher plant, insect and mammalian cells in culture) of exogenous DNA sequences obtained by genomic or cDNA cloning or by gene synthesis. That is, in a preferred embodiment, SCF is "recombinant SCF." The products of expression in typical yeast (e.g., Saccharomyces cerevisiae) or procaryote (e.g., E. coli) host cells are free of association with any mammalian proteins. The products of expression in vertebrate [e.g., non-human mammalian (e.g. COS or CHO) and avian] cells are free of association with any human proteins. Depending upon the host employed, polypeptides of the invention may be glycosylated with mammalian or other eucaryotic carbohydrates or may be non-glycosylated. The host cell can be altered using techniques such as those described in Lee et al. J. Biol. Chem. 264, 13848 (1989) hereby incorporated by reference. Polypeptides of the invention may also include an initial methionine amino acid residue (at position -1).

In addition to naturally-occurring allelic forms of SCF, the present invention also embraces other SCF products such as polypeptide analogs of SCF. Such analogs include fragments of SCF. Following the procedures of the above-noted published application by Alton et al. (WO 83/04053), one can readily design and manufacture genes coding for microbial expression of polypeptides having primary conformations which differ from that herein specified for in terms of the identity or location of one or more residues (e.g., substitutions, terminal and intermediate additions and deletions). Alternately, modifications of cDNA and genomic genes can be readily accomplished by well-known

site-directed mutagenesis techniques and employed to generate analogs and derivatives of SCF. Such products share at least one of the biological properties of SCF but may differ in others. As examples, products of the invention include those which are foreshortened by e.g., deletions; or those which are more stable to hydrolysis (and, therefore, may have more pronounced or longer-lasting effects than naturally-occurring); or which have been altered to delete or to add one or more potential sites for O-glycosylation and/or N-glycosylation or which have one or more cysteine residues deleted or replaced by, e.g., alanine or serine residues and are potentially more easily isolated in active form from microbial systems; or which have one or more tyrosine residues replaced by phenylalanine and bind more or less readily to target proteins or to receptors on target cells. Also comprehended are polypeptide fragments duplicating only a part of the continuous amino acid sequence or secondary conformations within SCF, which fragments may possess one property of SCF (e.g., receptor binding) and not others (e.g., early hematopoietic cell growth activity). It is noteworthy that activity is not necessary for any one or more of the products of the invention to have therapeutic utility [see, Weiland et al., Blut, 44, 173-175 (1982)] or utility in other contexts, such as in assays of SCF antagonism. Competitive antagonists may be quite useful in, for example, cases of overproduction of SCF or cases of human leukemias where the malignant cells overexpress receptors for SCF, as indicated by the overexpression of SCF receptors in leukemic blasts (Example 13).

Of applicability to polypeptide analogs of the invention are reports of the immunological property of synthetic peptides which substantially duplicate the amino acid sequence extant in naturally-occurring proteins, glycoproteins and nucleoproteins. More

specifically, relatively low molecular weight polypeptides have been shown to participate in immune reactions which are similar in duration and extent to the immune reactions of physiologically-significant proteins such as viral antigens, polypeptide hormones, and the like. Included among the immune reactions of such polypeptides is the provocation of the formation of specific antibodies in immunologically-active animals [Lerner et al., Cell, 23, 309-310 (1981); Ross et al., Nature, 294, 654-656 (1981); Walter et al., Proc. Natl. Acad. Sci. USA, 77, 5197-5200 (1980); Lerner et al., Proc. Natl. Acad. Sci. USA, 78, 3403-3407 (1981); Walter et al., Proc. Natl. Acad. Sci. USA, 78, 4882-4886 (1981); Wong et al., Proc. Natl. Acad. Sci. USA, 79, 5322-5326 (1982); Baron et al., Cell, 28, 395-404 (1982); Dressman et al., Nature, 295, 185-160 (1982); and Lerner, Scientific American, 248, 66-74 (1983)]. See, also, Kaiser et al. [Science, 223, 249-255 (1984)] relating to biological and immunological properties of synthetic peptides which approximately share secondary structures of peptide hormones but may not share their primary structural conformation.

The present invention also includes that class of polypeptides coded for by portions of the DNA complementary to the protein-coding strand of the human cDNA or genomic DNA sequences of SCF, i.e., "complementary inverted proteins" as described by Tramontano et al. [Nucleic Acid Res., 12, 5049-5059 (1984)].

Representative SCF polypeptides of the present invention include but are not limited to SCF¹-148, SCF¹-162, SCF¹-164, SCF¹-165 and SCF¹-183 in Figure 15C; SCF¹-185, SCF¹-188, SCF¹-189 and SCF¹-248 in Figure 42; and SCF¹-157, SCF¹-160, SCF¹-161 and SCF¹-220 in Figure 44.

SCF can be purified using techniques known to those skilled in the art. The subject invention comprises a method of purifying SCF from an SCF containing material such as conditioned media or human
5 urine, serum, the method comprising one or more of steps such as the following: subjecting the SCF containing material to ion exchange chromatography (either cation or anion exchange chromatography); subjecting the SCF containing material to reverse phase liquid
10 chromatographic separation involving, for example, an immobilized C₄ or C₆ resin; subjecting the fluid to immobilized-lectin chromatography, i.e., binding of SCF to the immobilized lectin, and eluting with the use of a sugar that competes for this binding. Details in the
15 use of these methods will be apparent from the descriptions given in Examples 1, 10, and 11 for the purification of SCF. The techniques described in Example 2 of the Lai et al. U.S. patent 4,667,016, hereby incorporated by reference are also useful in
20 purifying stem cell factor.

Isoforms of SCF are isolated using standard techniques such as the techniques set forth in commonly owned U.S. Ser. No. 421,444 entitled Erythropoietin
Isoforms, filed October 13, 1989, hereby incorporated by
25 reference.

Also comprehended by the invention are pharmaceutical compositions comprising therapeutically effective amounts of polypeptide products of the invention together with suitable diluents,
30 preservatives, solubilizers, emulsifiers, adjuvants and/or carriers useful in SCF therapy. A "therapeutically effective amount" as used herein refers to that amount which provides a therapeutic effect for a given condition and administration regimen. Such
35 compositions are liquids or lyophilized or otherwise dried formulations and include diluents of various

buffer content (e.g., Tris-HCl., acetate, phosphate), pH and ionic strength, additives such as albumin or gelatin to prevent adsorption to surfaces, detergents (e.g., Tween 20, Tween 80, Pluronic F68, bile acid salts),
5 solubilizing agents (e.g., glycerol, polyethylene glycol), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimerosal, benzyl alcohol, parabens), bulking substances or tonicity modifiers (e.g., lactose, mannitol), covalent attachment
10 of polymers such as polyethylene glycol to the protein (described in Example 12 below), complexation with metal ions, or incorporation of the material into or onto particulate preparations of polymeric compounds such as =
polylactic acid, polglycolic acid, hydrogels, etc. or -
15 into liposomes, microemulsions, micelles, unilamellar or multilamellar vesicles, erythrocyte ghosts, or spheroplasts. Such compositions will influence the physical state, solubility, stability, rate of in vivo release, and rate of in vivo clearance of SCF. The
20 choice of composition will depend on the physical and chemical properties of the protein having SCF activity. For example, a product derived from a membrane-bound form of SCF may require a formulation containing detergent. Controlled or sustained release
25 compositions include formulation in lipophilic depots (e.g., fatty acids, waxes, oils). Also comprehended by the invention are particulate compositions coated with polymers (e.g., poloxamers or poloxamines) and SCF coupled to antibodies directed against tissue-specific
30 receptors, ligands or antigens or coupled to ligands of tissue-specific receptors. Other embodiments of the compositions of the invention incorporate particulate forms, protective coatings, protease inhibitors or permeation enhancers for various routes of
35 administration, including parenteral, pulmonary, nasal and oral.

The invention also comprises compositions including one or more additional hematopoietic factors such as EPO, G-CSF, GM-CSF, CSF-1, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IGF-I, or LIF (Leukemic Inhibitory Factor).

Polypeptides of the invention may be "labeled" by association with a detectable marker substance (e.g., radiolabeled with ^{125}I or biotinylated) to provide reagents useful in detection and quantification of SCF or its receptor bearing cells in solid tissue and fluid samples such as blood or urine.

Biotinylated SCF is useful in conjunction with immobilized streptavidin to purge leukemic blasts from bone marrow in autologous bone marrow transplantation. Biotinylated SCF is useful in conjunction with immobilized streptavidin to enrich for stem cells in autologous or allogeneic stem cells in autologous or allogeneic bone marrow transplantation. Toxin conjugates of SCF, such as ricin [Uhr, Prog. Clin. Biol. Res. 288, 403-412 (1989)] diphtheria toxin [Moolten, J. Natl. Con. Inst., 55, 473-477 (1975)], and radioisotopes are useful for direct anti-neoplastic therapy (Example 13) or as a conditioning regimen for bone marrow transplantation.

Nucleic acid products of the invention are useful when labeled with detectable markers (such as radiolabels and non-isotopic labels such as biotin) and employed in hybridization processes to locate the human SCF gene position and/or the position of any related gene family in a chromosomal map. They are also useful for identifying human SCF gene disorders at the DNA level and used as gene markers for identifying neighboring genes and their disorders. The human SCF gene is encoded on chromosome 12, and the murine SCF gene maps to chromosome 10 at the *S1* locus.

SCF is useful, alone or in combination with other therapy, in the treatment of a number of hematopoietic disorders. SCF can be used alone or with one or more additional hematopoietic factors such as

5 EPO, G-CSF, GM-CSF, CSF-1, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-1, IGF-I or LIF in the treatment of hematopoietic disorders.

There is a group of stem cell disorders which are characterized by a reduction in functional marrow

10 mass due to toxic, radiant, or immunologic injury and which may be treatable with SCF. Aplastic anemia is a stem cell disorder in which there is a fatty replacement of hematopoietic tissue and pancytopenia. SCF enhances hematopoietic proliferation and is useful in treating

15 aplastic anemia (Example 8B). Steel mice are used as a model of human aplastic anemia [Jones, Exp. Hematol., 11, 571-580 (1983)]. Promising results have been obtained with the use of a related cytokine, GM-CSF in the treatment of aplastic anemia [Antin, et al., Blood,

20 70, 129a (1987)]. Paroxysmal nocturnal hemoglobinuria (PNH) is a stem cell disorder characterized by formation of defective platelets and granulocytes as well as abnormal erythrocytes.

There are many diseases which are treatable

25 with SCF. These include the following: myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Siwe disease, refractory erythroblastic anemia,

30 Di Guglielmo syndrome, congestive splenomegaly, Hodgkin's disease, Kala azar, sarcoidosis, primary splenic pancytopenia, miliary tuberculosis, disseminated fungus disease, Fulminating septicemia, malaria, vitamin B₁₂ and folic acid deficiency, pyridoxine deficiency,

35 Diamond Blackfan anemia, hypopigmentation disorders such as piebaldism and vitiligo. The erythroid,

megakaryocyte, and granulocytic stimulatory properties of SCF are illustrated in Example 8B and 8C.

Enhancement of growth in non-hematopoietic stem cells such as primordial germ cells, neural crest derived melanocytes, commissural axons originating from the dorsal spinal cord, crypt cells of the gut, mesonephric and metanephric kidney tubules, and olfactory bulbs is of benefit in states where specific tissue damage has occurred to these sites. SCF is useful for treating neurological damage and is a growth factor for nerve cells. SCF is useful during in vitro fertilization procedures or in treatment of infertility states. SCF is useful for treating intestinal damage resulting from irradiation or chemotherapy.

There are stem cell myeloproliferative disorders such as polycythemia vera, chronic myelogenous leukemia, myeloid mataplasia, primary thrombocythemia, and acute leukemias which are treatable with SCF, anti-SCF antibodies, or SCF-toxin conjugates.

There are numerous cases which document the increased proliferation of leukemic cells to the hematopoietic cell growth factors G-CSF, GM-CSF, and IL-3 [Delwel, et al., Blood, 72, 1944-1949 (1988)]. Since the success of many chemotherapeutic drugs depends on the fact that neoplastic cells cycle more actively than normal cells, SCF alone or in combination with other factors acts as a growth factor for neoplastic cells and sensitizes them to the toxic effects of chemotherapeutic drugs. The overexpression of SCF receptors on leukemic blasts is shown in Example 13.

A number of recombinant hematopoietic factors are undergoing investigation for their ability to shorten the leukocyte nadir resulting from chemotherapy and radiation regimens. Although these factors are very useful in this setting, there is an early hematopoietic compartment which is damaged, especially by radiation,

and has to be repopulated before these later-acting growth factors can exert their optimal action. The use of SCF alone or in combination with these factors further shortens or eliminates the leukocyte and platelet nadir resulting from chemotherapy or radiation treatment. In addition, SCF allows for a dose intensification of the anti-neoplastic or irradiation regimen (Example 19).

SCF is useful for expanding early hematopoietic progenitors in syngeneic, allogeneic, or autologous bone marrow transplantation. The use of hematopoietic growth factors has been shown to decrease the time for neutrophil recovery after transplantation [Donahue, et al., Nature, 321, 872-875 (1986) and Welte et al., J. Exp. Med., 165, 941-948, (1987)]. For bone marrow transplantation, the following three scenarios are used alone or in combination: a donor is treated with SCF alone or in combination with other hematopoietic factors prior to bone marrow aspiration or peripheral blood leucaphoresis to increase the number of cells available for transplantation; the bone marrow is treated in vitro to activate or expand the cell number prior to transplantation; finally, the recipient is treated to enhance engraftment of the donor marrow.

SCF is useful for enhancing the efficiency of gene therapy based on transfecting (or infecting with a retroviral vector) hematopoietic stem cells. SCF permits culturing and multiplication of the early hematopoietic progenitor cells which are to be transfected. The culture can be done with SCF alone or in combination with IL-6, IL-3, or both. Once tranfected, these cells are then infused in a bone marrow transplant into patients suffering from genetic disorders. [Lim, Proc. Natl. Acad. Sci, 86, 8892-8896 (1989)]. Examples of genes which are useful in treating genetic disorders include adenosine deaminase, glucocerebrosidase, hemoglobin, and cystic fibrosis.

SCF is useful for treatment of acquired immune deficiency (AIDS) or severe combined immunodeficiency states (SCID) alone or in combination with other factors such as IL-7 (see Example 14). Illustrative of this effect is the ability of SCF therapy to increase the absolute level of circulating T-helper (CD4+, OKT₄+) lymphocytes. These cells are the primary cellular target of human immunodeficiency virus (HIV) leading to the immunodeficiency state in AIDS patients [Montagnier, in Human T-Cell Leukemia/Lymphoma Virus, ed. R.C. Gallo, Cold Spring Harbor, New York, 369-379 (1984)]. In addition, SCF is useful for combatting the myelosuppressive effects of anti-HIV drugs such as AZT [Gogu Life Sciences, 45, No. 4 (1989)].

SCF is useful for enhancing hematopoietic recovery after acute blood loss.

In vivo treatment with SCF is useful as a boost to the immune system for fighting neoplasia (cancer). An example of the therapeutic utility of direct immune function enhancement by a recently cloned cytokine (IL-2) is described in Rosenberg et al., N. Eng. J. Med., 313 1485 (1987).

The administration of SCF with other agents such as one or more other hematopoietic factors, is temporally spaced or given together. Prior treatment with SCF enlarges a progenitor population which responds to terminally-acting hematopoietic factors such as G-CSF or EPO. The route of administration may be intravenous, intraperitoneal sub-cutaneous, or intramuscular.

The subject invention also relates to antibodies specifically binding stem cell factor. Example 7 below describes the production of polyclonal antibodies. A further embodiment of the invention is monoclonal antibodies specifically binding SCF (see Example 20). In contrast to conventional antibody (polyclonal) preparations which typically include

different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. Monoclonal antibodies are useful to improve the
5 selectivity and specificity of diagnostic and analytical assay methods using antigen-antibody binding. Also, they are used to neutralize or remove SCF from serum. A second advantage of monoclonal antibodies is that they can be synthesized by hybridoma cells in culture,
10 uncontaminated by other immunoglobulins. Monoclonal antibodies may be prepared from supernatants of cultured hybridoma cells or from ascites induced by intra-peritoneal inoculation of hybridoma cells into mice. The hybridoma technique described originally by Köhler
15 and Milstein [Eur. J. Immunol. 6, 511-519 (1976)] has been widely applied to produce hybrid cell lines that secrete high levels of monoclonal antibodies against many specific antigens.

The following examples are offered to more
20 fully illustrate the invention, but are not to be construed as limiting the scope thereof.

EXAMPLE 1

Purification/Characterization of Stem Cell Factor 25 from Buffalo Rat Liver Cell Conditioned Medium

A. In Vitro Biological Assays

1. HPP-CFC Assay

30 There are a variety of biological activities which can be attributed to the natural mammalian rat SCF as well as the recombinant rat SCF protein. One such activity is its effect on early hematopoietic cells. This activity can be measured in a High Proliferative
35 Potential Colony Forming Cell (HPP-CFC) assay [Zsebo, et al., supra (1988)]. To investigate the effects of

factors on early hematopoietic cells, the HPP-CFC assay system utilizes mouse bone marrow derived from animals 2 days after 5-fluorouracil (5-FU) treatment. The chemotherapeutic drug 5-FU selectively depletes late
5 hematopoietic progenitors, allowing for detection of early progenitor cells and hence factors which act on such cells. The rat SCF is plated in the presence of CSF-1 or IL-6 in semi-solid agar cultures. The agar cultures contain McCoys complete medium (GIBCO), 20%
10 fetal bovine serum, 0.3% agar, and 2×10^5 bone marrow cells/ml. The McCoys complete medium contains the following components: 1xMcCoys medium supplemented with 0.1 mM pyruvate, 0.24x essential amino acids, 0.24x non-essential amino acids, 0.027% sodium bicarbonate, 0.24x
15 vitamins, 0.72 mM glutamine, 25 µg/ml L-serine, and 12 µg/ml L-asparagine. The bone marrow cells are obtained from Balb/c mice injected i.v. with 150 mg/kg 5-FU. The femurs are harvested 2 days post 5-FU treatment of the mice and bone marrow is flushed out.
20 The red blood cells are lysed with red blood cell lysing reagent (Becton Dickenson) prior to plating. Test substances are plated with the above mixture in 30 mm dishes. Fourteen days later the colonies (>1 mm in diameter) which contain thousands of cells are scored.
25 This assay was used throughout the purification of natural mammalian cell-derived rat SCF.

In a typical assay, rat SCF causes the proliferation of approximately 50 HPP-CFC per 200,000 cells plated. The rat SCF has a synergistic activity on
30 5-FU treated mouse bone marrow cells; HPP-CFC colonies will not form in the presence of single factors but the combination of SCF and CSF-1 or SCF and IL-6 is active in this assay.

2. MC/9 Assay

Another useful biological activity of both naturally-derived and recombinant rat SCF is the ability to cause the proliferation of the IL-4 dependent murine mast cell line, MC/9 (ATCC CRL 8306). MC/9 cells are cultured with a source of IL-4 according to the ATCC CRL 8306 protocol. The medium used in the bioassay is RPMI 1640, 4% fetal bovine serum, $5 \times 10^{-5} \text{M}$ 2-mercaptoethanol, and 1x glutamine-pen-strep. The MC/9 cells proliferate in response to SCF without the requirement for other growth factors. This proliferation is measured by first culturing the cells for 24 h without growth factors, plating 5000 cells in each well of 96 well plates with test sample for 48h, pulsing for 4 h with 0.5 uCi ^3H -thymidine (specific activity 20 Ci/mmol), harvesting the solution onto glass fiber filters, and then measuring specifically-bound radioactivity. This assay was used in the purification of mammalian cell derived rat SCF after the ACA 54 gel filtration step, section C2 of this Example. Typically, SCF caused a 4-10 fold increase in CPM over background.

3. CFU-GM

The action of purified mammalian SCF, both naturally-derived and recombinant, free from interfering colony stimulating factors (CSFs), on normal undepleted mouse bone marrow has been ascertained. A CFU-GM assay [Broxmeyer et al. Exp. Hematol., 5, 87 (1977)] is used to evaluate the effect of SCF on normal marrow. Briefly, total bone marrow cells after lysis of red blood cells are plated in semi-solid agar cultures containing the test substance. After 10 days, the colonies containing clusters of >40 cells are scored. The agar cultures can be dried down onto glass slides and the morphology of the cells can be determined via specific histological stains.

On normal mouse bone marrow, the purified mammalian rat SCF was a pluripotential CSF, stimulating the growth of colonies consisting of immature cells, neutrophils, macrophages, eosinophils, and megakaryocytes without the requirement for other factors. From 200,000 cells plated, over 100 such colonies grow over a 10 day period. Both rat and human recombinant SCF stimulate the production of erythroid cells in combination with EPO, see Example 9.

10

B. Conditioned Medium

Buffalo rat liver (BRL) 3A cells, from the American Type Culture Collection (ATCC CRL 1442), were grown on microcarriers in a 20 liter perfusion culture system for the production of SCF. This system utilizes a Biolafitte fermenter (Model ICC-20) except for the screens used for retention of microcarriers and the oxygenation tubing. The 75 micron mesh screens are kept free of microcarrier clogging by periodic back flushing achieved through a system of check valves and computer-controlled pumps. Each screen alternately acts as medium feed and harvest screen. This oscillating flow pattern ensures that the screens do not clog. Oxygenation was provided through a coil of silicone tubing (50 feet long, 0.25 inch ID, 0.03 inch wall). The growth medium used for the culture of BRL 3A cells was Minimal Essential Medium (with Earle's Salts) (GIBCO), 2 mM glutamine, 3 g/L glucose, tryptose phosphate (2.95 g/L), 5% fetal bovine serum and 5% fetal calf serum. The harvest medium was identical except for the omission of serum. The reactor contained Cytodex 2 microcarriers (Pharmacia) at a concentration of 5 g/L and was seeded with 3×10^9 BRL 3A cells grown in roller bottles and removed by trypsinization. The cells were allowed to attach to and grow on the microcarriers for eight days.

Growth medium was perfused through the reactor as needed based on glucose consumption. The glucose concentration was maintained at approximately 1.5 g/L. After eight days, the reactor was perfused with six volumes of serum free medium to remove most of the serum (protein concentration < 50 ug/ml). The reactor was then operated batchwise until the glucose concentration fell below 2 g/L. From this point onward, the reactor was operated at a continuous perfusion rate of approximately 10 L/day. The pH of the culture was maintained at 6.9 ± 0.3 by adjusting the CO₂ flow rate. The dissolved oxygen was maintained higher than 20% of air saturation by supplementing with pure oxygen as necessary. The temperature was maintained at $37 \pm 0.5^\circ\text{C}$.

Approximately 336 liters of serum free conditioned medium was generated from the above system and was used as the starting material for the purification of natural mammalian cell-derived rat SCF.

C. Purification

All purification work was carried out at 4°C unless indicated otherwise.

1. DEAE-cellulose Anion Exchange Chromatography

Conditioned medium generated by serum-free growth of BRL 3A cells was clarified by filtration through 0.45 μ Sartocapsules (Sartorius). Several different batches (41 L, 27 L, 39 L, 30.2 L, 37.5 L, and 161 L) were separately subjected to concentration, diafiltration/buffer exchange, and DEAE-cellulose anion exchange chromatography, in similar fashion for each batch. The DEAE-cellulose pools were then combined and processed further as one batch in sections C2-5 of this Example. To illustrate, the handling of the 41 L batch was as follows. The filtered conditioned medium was

concentrated to ~700 ml using a Millipore Pellicon tangential flow ultrafiltration apparatus with four 10,000 molecular weight cutoff polysulfone membrane cassettes (20 ft² total membrane area; pump rate ~1095 ml/min and filtration rate 250-315 ml/min). Diafiltration/buffer exchange in preparation for anion exchange chromatography was then accomplished by adding 500 ml of 50 mM Tris-HCl, pH 7.8 to the concentrate, reconcentrating to 500 ml using the tangential flow ultrafiltration apparatus, and repeating this six additional times. The concentrated/diafiltered preparation was finally recovered in a volume of 700 ml. The preparation was applied to a DEAE-cellulose anion exchange column (5 x 20.4 cm; Whatman DE-52 resin) which had been equilibrated with the 50 mM Tris-HCl, pH 7.8 buffer. After sample application, the column was washed with 2050 ml of the Tris-HCl buffer, and a salt gradient (0-300 mM NaCl in the Tris-HCl buffer; 4 L total volume) was applied. Fractions of 15 ml were collected at a flow rate of 167 ml/h. The chromatography is shown in Figure 1. HPP-CFC colony number refers to biological activity in the HPP-CFC assay; 100 µl from the indicated fractions was assayed. Fractions collected during the sample application and wash are not shown in the Figure; no biological activity was detected in these fractions.

The behavior of all conditioned media batches subjected to the concentration, diafiltration/buffer exchange, and anion exchange chromatography was similar. Protein concentrations for the batches, determined by the method of Bradford [Anal. Biochem. 72, 248-254 (1976)] with bovine serum albumin as standard were in the range 30-50 µg/ml. The total volume of conditioned medium utilized for this preparation was about 336 L.

2. ACA 54 Gel Filtration Chromatography

Fractions having biological activity from the DEAE-cellulose columns run for each of the six conditioned media batches referred to above (for example, fractions 87-114 for the run shown in Figure 1) were combined (total volume 2900 ml) and concentrated to a final volume of 74 ml with the use of Amicon stirred cells and YM10 membranes. This material was applied to an ACA 54 (LKB) gel filtration column (Figure 2) equilibrated in 50 mM Tris-HCl, 50 mM NaCl, pH 7.4. Fractions of 14 ml were collected at a flow rate of 70 ml/h. Due to inhibitory factors co-eluting with the active fractions, the peak of activity (HPP-CFC colony number) appears split; however, based on previous chromatograms, the activity co-elutes with the major protein peak and therefore one pool of the fractions was made.

3. Wheat Germ Agglutinin-Agarose Chromatography

Fractions 70-112 from the ACA 54 gel filtration column were pooled (500 ml). The pool was divided in half and each half subjected to chromatography using a wheat germ agglutinin-agarose column (5 x 24.5 cm; resin from E-Y Laboratories, San Mateo, CA; wheat germ agglutinin recognizes certain carbohydrate structures) equilibrated in 20 mM Tris-HCl, 500 mM NaCl, pH 7.4. After the sample applications, the column was washed with about 2200 ml of the column buffer, and elution of bound material was then accomplished by applying a solution of 350 mM N-acetyl-D-glucosamine dissolved in the column buffer, beginning at fraction -210 in Figure 3. Fractions of 13.25 ml were collected at a flow rate of 122 ml/h. One of the chromatographic runs is shown in Figure 3. Portions of the fractions to be assayed were dialyzed against phosphate-buffered saline; 5 ul of the dialyzed

materials were placed into the MC/9 assay (cpm values in Figure 3) and 10 μ l into the HPP-CFC assay (colony number values in Figure 3). It can be seen that the active material bound to the column and was eluted with the N-acetyl-D-glucosamine, whereas much of the contaminating material passed through the column during sample application and wash.

4. S-Sepharose Fast Flow Cation Exchange Chromatography

Fractions 211-225 from the wheat germ agglutinin-agarose chromatography shown in Figure 3 and equivalent fractions from the second run were pooled (375 ml) and dialyzed against 25 mM sodium formate, pH 4.2. To minimize the time of exposure to low pH, the dialysis was done over a period of 8 h, against 5 L of buffer, with four changes being made during the 8 h period. At the end of this dialysis period, the sample volume was 480 ml and the pH and conductivity of the sample were close to those of the dialysis buffer. Precipitated material appeared in the sample during dialysis. This was removed by centrifugation at 22,000 x g for 30 min, and the supernatant from the centrifuged sample was applied to a S-Sepharose Fast Flow cation exchange column (3.3 x 10.25 cm; resin from Pharmacia) which had been equilibrated in the sodium formate buffer. Flow rate was 465 ml/h and fractions of 14.2 ml were collected. After sample application, the column was washed with 240 ml of column buffer and elution of bound material was carried out by applying a gradient of 0-750 mM NaCl (NaCl dissolved in column buffer; total gradient volume 2200 ml), beginning at fraction -45 in Figure 4. The elution profile is shown in Figure 4. Collected fractions were adjusted to pH 7-7.4 by addition of 200 μ l of 0.97 M Tris base. The cpm in Figure 4 again refer to the results obtained in the MC/9 biological assay; portions of the indicated

fractions were dialyzed against phosphate-buffered saline, and 20 μ l placed into the assay. It can be seen in Figure 4 that the majority of biologically active material passed through the column unbound, whereas much of the contaminating material bound and was eluted in the salt gradient.

5. Chromatography Using Silica-Bound Hydrocarbon Resin

Fractions 4-40 from the S-Sepharose column of Figure 4 were pooled (540 ml). 450 ml of the pool was combined with an equal volume of buffer B (100 mM ammonium acetate, pH 6:isopropanol; 25:75) and applied at a flow rate of 540 ml/h to a C₄ column (Vydac Proteins C₄; 2.4 x 2 cm) equilibrated with buffer A (60 mM ammonium acetate, pH 6:isopropanol; 62.5:37.5). After sample application, the flow rate was reduced to 154 ml/h and the column was washed with 200 ml of buffer A. A linear gradient from buffer A to buffer B (total volume 140 ml) was then applied, and fractions of 9.1 ml were collected. Portions of the pool from S-Sepharose chromatography, the C₄ column starting sample, runthrough pool, and wash pool were brought to 40 μ g/ml bovine serum albumin by addition of an appropriate volume of a 1 mg/ml stock solution, and dialyzed against phosphate-buffered saline in preparation for biological assay. Similarly, 40 μ l aliquots of the gradient fractions were combined with 360 μ l of phosphate-buffered saline containing 16 μ g bovine serum albumin, and this was followed by dialysis against phosphate-buffered saline in preparation for biological assay. These various fractions were assayed by the MC/9 assay (6.3 μ l aliquots of the prepared gradient fractions; cpm in Figure 5). The assay results also indicated that about 75% of the recovered activity was in the runthrough and wash fractions, and 25% in the gradient fractions indicated in Figure 5. SDS-PAGE

[Laemmli, Nature, 227, 680-685 (1970); stacking gels contained 4% (w/v) acrylamide and separating gels contained 12.5% (w/v) acrylamide] of aliquots of various fractions is shown in Figure 6. For the gel shown, sample aliquots were dried under vacuum and then redissolved using 20 μ l sample treatment buffer (nonreducing, i.e., without 2-mercaptoethanol) and boiled for 5 min prior to loading onto the gel. Lanes A and B represent column starting material (75 μ l out of 890 ml) and column runthrough (75 μ l out of 880 ml), respectively; the numbered marks at the left of the Figure represent migration positions (reduced) of markers having molecular weights of 10^3 times the indicated numbers, where the markers are phosphorylase b (M_r of 97,400), bovine serum albumin (M_r of 66,200), ovalbumin (M_r of 42,700), carbonic anhydrase (M_r of 31,000), soybean trypsin inhibitor (M_r of 21,500), and lysozyme (M_r of 14,400); lanes 4-9 represent the corresponding fractions collected during application of the gradient (60 μ l out of 9.1 ml). The gel was silver-stained [Morrissey, Anal. Biochem., 117, 307-310 (1981)]. It can be seen by comparing lanes A and B that the majority of stainable material passes through the column. The stained material in fractions 4-6 in the regions just above and below the M_r 31,000 standard position coincides with the biological activity detected in the gradient fractions (Figure 5) and represents the biologically active material. It should be noted that this material is visualized in lanes 4-6, but not in lanes A and/or B, because a much larger proportion of the total volume (0.66% of the total for fractions 4-6 versus 0.0084% of the total for lanes A and B) was loaded for the former. Fractions 4-6 from this column were pooled.

As mentioned above, roughly 75% of the recovered activity ran through the C_4 column of

Figure 5. This material was rechromatographed using C₄ resin essentially as described above, except that a larger column (1.4 x 7.8 cm) and slower flow rate (50-60 ml/h throughout) were used. Roughly 50% of recovered activity was in the runthrough, and 50% in gradient fractions showing similar appearance on SDS-PAGE to that of the active gradient fractions in Figure 6. Active fractions were pooled (29 ml).

An analytical C₄ column was also performed essentially as stated above and the fractions were assayed in both bioassays. As indicated in Figure 7 of the fractions from this analytical column, both the MC/9 and HPP-CFC bioactivities co-elute. SDS-PAGE analysis (Figure 8) reveals the presence of the M_r ~31,000 protein in the column fractions which contain biological activity in both assays.

Active material in the second (relatively minor) activity peak seen in S-Sepharose chromatography (e.g. Figure 4, fractions 62-72, early fractions in the salt gradient) has also been purified by C₄ chromatography. It exhibited the same behavior on SDS-PAGE and had the same N-terminal amino acid sequence (see Example 2D) as the material obtained by C₄ chromatography of the S-Sepharose runthrough fractions.

6. Purification Summary

A summary of the purification steps described in 1-5 above is given in Table 2.

Table 2
Summary of Purification of Mammalian SCF

5	Step	Total	
		Volume (ml)	Protein (mg) ⁵
	Conditioned medium	335,700	13,475
	DEAE cellulose ¹	2,900	2,164
	ACA-54	550	1,513
10	Wheat germ agglutinin-agarose ²	375	431
	S-Sepharose	540 ⁴	10
	C ₄ resin ³	57.3	0.25-0.40 ⁶
<hr/>			
	1. Values given represent sums of the values for the different batches described in the text.		
15	2. As described above in this Example, precipitated material which appeared during dialysis of this sample in preparation for S-Sepharose chromatography was removed by centrifugation. The sample after centrifugation (480 ml) contained 264 mg of total protein.		
20	3. Combination of the active gradient fractions from the two C ₄ columns run in sequence as described.		
	4. Only 450 ml of this material was used for the following step (this Example, above).		
25	5. Determined by the method of Bradford (supra, 1976) except where indicated otherwise.		
	6. Estimate, based on intensity of silver-staining after SDS-PAGE, and on amino acid composition analysis as described in section K of Example 2.		

30 D. SDS-PAGE and Glycosidase Treatments

SDS-PAGE of pooled gradient fractions from the two large scale C₄ column runs are shown in Figure 9. Sixty μ l of the pool for the first C₄ column was loaded (lane 1), and 40 μ l of the pool for the second C₄ column (lane 2). These gel lanes were silver-stained.

Molecular weight markers were as described for Figure 6. As mentioned, the diffusely-migrating material above and below the M_r 31,000 marker position represents the biologically active material; the
5 apparent heterogeneity is largely due to heterogeneity in glycosylation.

To characterize the glycosylation, purified material was iodinated with ^{125}I , treated with a variety of glycosidases, and analyzed by SDS-PAGE (reducing
10 conditions) with autoradiography. Results are shown in Figure 9. Lanes 3 and 9, ^{125}I -labeled material without any glycosidase treatment. Lanes 4-8 represent ^{125}I -labeled material treated with glycosidases, as follows. Lane 4, neuraminidase. Lane 5, neuraminidase
15 and O-glycanase. Lane 6, N-glycanase. Lane 7, neuraminidase and N-glycanase. Lane 8, neuraminidase, O-glycanase, and N-glycanase. Conditions were 5 mM 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate (CHAPS), 33 mM 2-mercaptoethanol, 10 mM Tris-HCl,
20 pH 7-7.2, for 3 h at 37°C. Neuraminidase (from Arthrobacter ureafaciens; Calbiochem) was used at 0.23 units/ml final concentration. O-Glycanase (Genzyme; endo-alpha-N-acetyl-galactosaminidase) was used at 45 milliunits/ml. N-Glycanase (Genzyme;
25 peptide:N-glycosidase F; peptide- N^4 [N-acetyl-beta-glucosaminy]asparagine amidase) was used at 10 units/ml.

Similar results to those of Figure 9 were obtained upon treatment of unlabeled purified SCF with
30 glycosidases, and visualization of products by silver-staining after SDS-PAGE.

Where appropriate, various control incubations were carried out. These included: incubation in appropriate buffer, but without glycosidases, to verify
35 that results were due to the glycosidase preparations added; incubation with glycosylated proteins (e.g.

glycosylated recombinant human erythropoietin) known to be substrates for the glycosidases, to verify that the glycosidase enzymes used were active; and incubation with glycosidases but no substrate, to verify that the glycosidases were not themselves contributing to or obscuring the visualized gel bands.

Glycosidase treatments were also carried out with endo-beta-N-acetylglucosamidase F (endo F; NEN Dupont) and with endo-beta-N-acetylglucosaminidase H (endo H; NEN Dupont), again with appropriate control incubations. Conditions of treatment with endo F were: boiling 3 min in the presence of 1% (w/v) SDS, 100 mM 2-mercaptoethanol, 100 mM EDTA, 320 mM sodium phosphate, pH 6, followed by 3-fold dilution with the inclusion of Nonidet P-40 (1.17%, v/v, final concentration), sodium phosphate (200 mM, final concentration), and endo F (7 units/ml, final concentration). Conditions of endo H treatment were similar except that SDS concentration was 0.5% (w/v) and endo H was used at a concentration of 1 µg/ml. The results with endo F were the same as those with N-glycanase, whereas endo H had no effect on the purified SCF material.

A number of conclusions can be drawn from the glycosidase experiments described above. The various treatments with N-glycanase [which removes both complex and high-mannose N-linked carbohydrate (Tarentino et al., Biochemistry 24, 4665-4671) (1985)], endo F [which acts similarly to N-glycanase (Elder and Alexander, Proc. Natl. Acad. Sci. USA 79, 4540-4544 (1982)], endo H [which removes high-mannose and certain hybrid type N-linked carbohydrate (Tarentino et al., Methods Enzymol. 50C, 574-580 (1978)], neuraminidase (which removes sialic acid residues), and O-glycanase [which removes certain O-linked carbohydrates (Lambin et al., Biochem. Soc. Trans. 12, 599-600 (1984))], suggest that: both N-linked and O-linked carbohydrates

are present; most of the N-linked carbohydrate is of the complex type; and sialic acid is present, with at least some of it being part of the O-linked moieties. Some information about possible sites of N-linkage can be
5 obtained from amino acid sequence data (Example 2). The fact that treatment with N-glycanase, endo F, and N-glycanase/neuraminidase can convert the heterogeneous material apparent by SDS-PAGE to faster-migrating forms which are much more homogeneous is consistent with the
10 conclusion that all of the material represents the same polypeptide, with the heterogeneity being caused by heterogeneity in glycosylation. It is also noteworthy that the smallest forms obtained by the combined treatments with the various glycosidases are in the
15 range of M_r 18,000-20,000, relative to the molecular weight markers used in the SDS-PAGE.

Confirmation that the diffusely-migrating material around the M_r 31,000 position on SDS-PAGE represents biologically active material all having the
20 same basic polypeptide chain is given by the fact that amino acid sequence data derived from material migrating in this region (e.g., after electrophoretic transfer and cyanogen bromide treatment; Example 2) matches that demonstrated for the isolated gene whose expression by
25 recombinant DNA means leads to biologically-active material (Example 4).

EXAMPLE 2

30 Amino Acid Sequence Analysis of Mammalian SCF

A. Reverse-phase High Performance Liquid Chromatography (HPLC) of Purified Protein

35 Approximately 5 μ g of SCF purified as in Example 1 (concentration = 0.117 mg/ml) was subjected to

reverse-phase HPLC using a C₄ narrowbore column (Vydac, 300 Å widebore, 2 mm x 15 cm). The protein was eluted with a linear gradient from 97% mobile phase A (0.1% trifluoroacetic acid)/3% mobile phase B (90% acetonitrile in 0.1% trifluoroacetic acid) to 30% mobile phase A/70% mobile phase B in 70 min followed by isocratic elution for another 10 min at a flow rate of 0.2 ml per min. After subtraction of a buffer blank chromatogram, the SCF was apparent as a single symmetrical peak at a retention time of 70.05 min as shown in Figure 10. No major contaminating protein peaks could be detected under these conditions.

15 B. Sequencing of Electrophoretically-Transferred Protein Bands

SCF purified as in Example 1 (0.5-1.0 nmol) was treated as follows with N-glycanase, an enzyme which specifically cleaves the Asn-linked carbohydrate moieties covalently attached to proteins (see Example 1D). Six ml of the pooled material from fractions 4-6 of the C₄ column of Figure 5 was dried under vacuum. Then 150 µl of 14.25 mM CHAPS, 100 mM 2-mercaptoethanol, 335 mM sodium phosphate, pH 8.6 was added and incubation carried out for 95 min at 37°C. Next 300 µl of 74 mM sodium phosphate, 15 units/ml N-glycanase, pH 8.6 was added and incubation continued for 19 h. The sample was then run on a 9-18% SDS-polyacrylamide gradient gel (0.7 mm thickness, 20x20 cm). Protein bands in the gel were electrophoretically transferred onto polyvinylidene difluoride (PVDF, Millipore Corp.) using 10 mM Caps buffer (pH 10.5) at a constant current of 0.5 Amp for 1 h [Matsudaira, J. Biol. Chem., 261, 10035-10038 (1987)]. The transferred protein bands were visualized by Coomassie Blue staining. Bands were present at M_r ~29,000-33,000 and M_r ~26,000, i.e., the

deglycosylation was only partial (refer to Example 1D, Figure 9); the former band represents undigested material and the latter represents material from which N-linked carbohydrate is removed. The bands were cut
5 out and directly loaded (40% for M_r 29,000-33,000 protein and 80% for M_r 26,000 protein) onto a protein sequencer (Applied Biosystems Inc., model 477). Protein sequence analysis was performed using programs supplied by the manufacturer [Hewick et al., J. Biol. Chem., 256
10 7990-7997 (1981)] and the released phenylthiohydantoinyl amino acids were analyzed on-line using microbore C_{18} reverse-phase HPLC. Both bands gave no signals for 20-28 sequencing cycles, suggesting that both were
unsequenceable by methodology using Edman chemistry. - -

15 The background level on each sequencing run was between 1-7 pmol which was far below the protein amount present in the bands. These data suggested that protein in the bands was N-terminally blocked.

20 C. In-situ CNBr Cleavage of Electrophoretically-Transferred Protein and Sequencing

To confirm that the protein was in fact blocked, the membranes were removed from the sequencer
25 (part B) and in situ cyanogen bromide (CNBr) cleavage of the blotted bands was carried out [CNBr (5%, w/v) in 70% formic acid for 1 h at 45°C] followed by drying and sequence analysis. Strong sequence signals were detected, representing internal peptides obtained from
30 methionyl peptide bond cleavage by CNBr.

Both bands yielded identical mixed sequence signals listed below for the first five cycles.

Amino Acids Identified

Cycle 1: Asp; Glu; Val; Ile; Leu
Cycle 2: Asp; Thr; Glu; Ala; Pro; Val
5 Cycle 3: Asn; Ser; His; Pro; Leu
Cycle 4: Asp; Asn; Ala; Pro; Leu
Cycle 5: Ser; Tyr; Pro

10 Both bands also yielded similar signals up to 20
cycles. The initial yields were 40-115 pmol for the M_r
26,000 band and 40-150 pmol for the M_r 29,000-33,000
band. These values are comparable to the original molar =
amounts of protein loaded onto the sequencer. The - -
15 results confirmed that protein bands corresponding to
SCF contained a blocked N-terminus. Procedures used to
obtain useful sequence information for N-terminally
blocked proteins include: (a) deblocking the N-terminus
(see section D); and (b) generating peptides by internal
20 cleavages by CNBr (see Section E), by trypsin (see
Section F), and by Staphylococcus aureus (strain V-8)
protease (Glu-C) (see Section G). Sequence analysis can
proceed after the blocked N-terminal amino acid is
removed or the peptide fragments are isolated. Examples
25 are described in detail below.

D. Sequence Analysis of BRL Stem Cell Factor Treated
with Pyroglutamic Acid Aminopeptidase

30 The chemical nature of the blockage moiety
present at the amino terminus of SCF was difficult to
predict. Blockage can be post-translational in vivo
[F. Wold, Ann. Rev. Biochem., 50, 783-814 (1981)] or may
occur in vitro during purification. Two post-
35 translational modifications are most commonly
observed. Acetylation of certain N-terminal amino acids

such as Ala, Ser, etc. can occur, catalyzed by N- α -acetyl transferase. This can be confirmed by isolation and mass spectrometric analysis of an N-terminally blocked peptide. If the amino terminus of a protein is
5 glutamine, deamidation of its gamma-amide can occur. Cyclization involving the gamma-carboxylate and the free N-terminus can then occur to yield pyroglutamate. To detect pyroglutamate, the enzyme pyroglutamate
10 aminopeptidase can be used. This enzyme removes the pyroglutamate residue, leaving a free amino terminus starting at the second amino acid. Edman chemistry can then be used for sequencing.

SCF (purified as in Example 1; 400 pmol) in 50 mM sodium phosphate buffer (pH 7.6 containing
15 dithiothreitol and EDTA) was incubated with 1.5 units of calf liver pyroglutamic acid aminopeptidase (pE-AP) for 16 h at 37°C. After reaction the mixture was directly loaded onto the protein sequencer. A major sequence
20 could be identified through 46 cycles. The initial yield was about 40% and repetitive yield was 94.2%. The N-terminal sequence of SCF including the N-terminal pyroglutamic acid is:

pE-AP cleavage site
25 + 10
pyroGlu-Glu-Ile-Cys-Arg-Asn-Pro-Val-Thr-Asp-Asn-Val-Lys-Asp-Ile-Thr-Lys-
20 30
Leu-Val-Ala-Asn-Leu-Pro-Asn-Asp-Tyr-Met-Ile-Thr-Leu-Asn-Tyr-Val-
30
40
Ala-Gly-Met-Asp-Val-Leu-Pro-Ser-His-xxx-Trp-Leu-Arg-Asp-.....
xxx, not assigned at position 43

35 These results indicated that SCF contains pyroglutamic acid as its N-terminus.

E. Isolation and Sequence Analysis of CNBr Peptides

SCF purified as in Example 1 (20-28 µg;
1.0-1.5 nmol) was treated with N-glycanase as described
5 in Example 1. Conversion to the M_r 26,000 material was
complete in this case. The sample was dried and
digested with CNBr in 70% formic acid (5%) for 18 h at
room temperature. The digest was diluted with water,
dried, and redissolved in 0.1% trifluoroacetic acid.
10 CNBr peptides were separated by reverse-phase HPLC using
a C₄ narrowbore column and elution conditions identical
to those described in Section A of this Example.
Several major peptide fractions were isolated and
sequenced, and the results are summarized in the
15 following:

20

25

30

35

	Peptide	Retention Time (min)	Sequence ⁴
5	CB-4	15.5	L-P-P---
	CB-6 ¹	22.1	a. I-T-L-N-Y-V-A-G-(M) b. V-A-S-D-T-S-D-C-V-L-S-_-_-L-G-P-E-K-D- S-R-V-S-V-(_-)-K----
10	CB-8	28.0	D-V-L-P-S-H-C-W-L-R-D-(M)
	CB-10	30.1	(containing sequence of CB-8)
	CB-15 ²	43.0	E-E-N-A-P-K-N-V-K-E-S-L-K-K-P-T-R-(N)-F-- T-P-E-E-F-F-S-I-F-D ³ -R-S-I-D-A-----
15	CB-14	37.3	
	and		
	CB-16		Both peptides contain identical sequence to CB-15
20			

1. Amino acids were not detected at positions 12, 13 and 25. Peptide b was not sequenced to the end.
2. (N) in CB-15 was not detected; it was inferred based on the potential N-linked glycosylation site. The peptide was not sequenced to the end.
3. Designates site where Asn may have been converted into Asp upon N-glycanase removal of N-linked sugar.
4. Single letter code was used: A,Ala; C,Cys; D,Asp; E,Glu; F,Phe; G,Gly; H,His; I,Ile; K,Lys; L,Leu; M,Met; N,Asn; P,Pro; Q,Gln; R,Arg; S,Ser; T,Thr; V,Val; W,Trp; and Y,Tyr.

F. Isolation and Sequencing of BRL Stem Cell Factor
Tryptic Fragments

SCF purified as in Example 1 (20 µg in 150 µl 0.1 M ammonium bicarbonate) was digested with 1 µg of trypsin at 37°C for 3.5 h. The digest was immediately run on reverse-phase narrow bore C₄ HPLC using elution conditions identical to those described in Section A of this Example. All eluted peptide peaks had retention times different from that of undigested SCF (Section A). The sequence analyses of the isolated peptides are shown below:

Peptide	Retention		Sequence
	Time	(min)	
T-1	7.1		E-S-L-K-K-P-E-T-R
T-2 ¹	28.1		V-S-V-()-K
T-3	32.4		I-V-D-D-L-V-A-A-M-E-E-N-A-P-K
T-4 ²	40.0		N-F-T-P-E-E-F-F-S-I-F-()-R
T-5 ³	46.4	a.	L-V-A-N-L-P-N-D-Y-M-I-T-L-N-Y-V-A-G-M-D-V-L-P-S-H-C-W-L-R
		b.	S-I-D-A-F-K-D-F-M-V-A-S-D-T-S-D-C-V-L-S-()-()-L-G----
T-7 ⁴	72.8		E-S-L-K-K-P-E-T-R-(N)-F-T-P-E-E-F-F-S-I-F-()-R
T-8	73.6		E-S-L-K-K-P-E-T-R-N-F-T-P-E-E-F-F-S-I-F-D-R

1. Amino acid at position 4 was not assigned.
2. Amino acid at position 12 was not assigned.
3. Amino acids at positions 20 and 21 in 6 of peptide T-5 were not identified; they were tentatively assigned as O-linked sugar attachment sites.
4. Amino acid at position 10 was not detected; it was inferred as Asn based on the potential N-linked glycosylation site. Amino acid at position 21 was not detected.

G. Isolation and Sequencing of BRL Stem Cell Factor
Peptides after S. aureus Glu-C Protease Cleavage

SCF purified as in Example 1 (20 µg in
5 150 µl 0.1 M ammonium bicarbonate) was subjected to
Glu-C protease cleavage at a protease-to-substrate ratio
of 1:20. The digestion was accomplished at 37°C for
18 h. The digest was immediately separated by reverse-
phase narrowbore C₄ HPLC. Five major peptide fractions
10 were collected and sequenced as described below:

	Retention		Sequence
	Peptides	Time (min)	
15	S-1	5.1	N-A-P-K-N-V-K-E
	S-2 ¹	27.7	S-R-V-S-V-()-K-P-F-M-L-P-P-V-A-(A)
	S-3 ²	46.3	No sequence detected
20	S-5 ³	71.0	S-L-K-K-P-E-T-R-N-F-T-P-E-E-F-F-S-I-F- (N)-R-S-I-D-A-F-K-D-F-M-V-A-S-D
	S-6 ³	72.6	S-L-K-K-P-E-T-R-N-F-T-P-E-E-F-F-S-I-F- (N)-R-S-I-D-A-F-K-D-F-M-V-A-S-D-T-S-D

25

1. Amino acid at position 6 of S-2 peptide was not
assigned; this could be an O-linked sugar
attachment site. The Ala at position 16 of S-2
30 peptide was detected in low yield.
2. Peptide S-3 could be the N-terminally blocked
peptide derived from the N-terminus of SCF.
3. N in parentheses was assigned as a potential
N-linked sugar attachment site.

35

H. Sequence Analysis of BRL Stem Cell Factor after BNPS-skatole Cleavage

SCF (2 µg) in 10 mM ammonium bicarbonate was
5 dried to completeness by vacuum centrifugation and then
redissolved in 100 µl of glacial acetic acid. A 10-20
fold molar excess of BNPS-skatole was added to the
solution and the mixture was incubated at 50°C for
60 min. The reaction mixture was then dried by vacuum
10 centrifugation. The dried residue was extracted with
100 µl of water and again with 50 µl of water. The
combined extracts were then subjected to sequence
analysis as described above. The following sequence was =
detected: - -

15 1 10
Leu-Arg-Asp-Met-Val-Thr-His-Leu-Ser-Val-Ser-Leu-Thr-Thr-Leu-Leu-
20 30
Asp-Lys-Phe-Ser-Asn-Ile-Ser-Glu-Gly-Leu-Ser-(Asn)-Tyr-Ser-Ile-Ile-
40
20 Asp-Lys-Leu-Gly-Lys-Ile-Val-Asp----

Position 28 was not positively assigned; it was assigned
as Asn based on the potential N-linked glycosylation
site.

25

I. C-Terminal Amino Acid Determination of BRL Stem Cell Factor

An aliquot of SCF protein (500 pmol) was
30 buffer-exchanged into 10 mM sodium acetate, pH 4.0
(final volume of 90 µl) and Brij-35 was added to 0.05%
(w/v). A 5 µl aliquot was taken for quantitation of
protein. Forty µl of the sample was diluted to 100 µl
with the buffer described above. Carboxypeptidase P
35 (from Penicillium janthinellum) was added at an enzyme-
to-substrate ratio of 1:200. The digestion proceeded at

25°C and 20 µl aliquots were taken at 0, 15, 30, 60 and 120 min. The digestion was terminated at each time point by adding trifluoroacetic acid to a final concentration of 5%. The samples were dried and the released amino acids were derivatized by reaction with Dabsyl chloride (dimethylaminoazobenzenesulfonyl chloride) in 0.2 M NaHCO₃ (pH 9.0) at 70°C for 12 min [Chang et al., Methods Enzymol., 90, 41-48 (1983)]. The derivatized amino acids (one-sixth of each sample) were analyzed by narrowbore reverse-phase HPLC with a modification of the procedure of Chang et al. [Techniques in Protein Chemistry, T. Hugli ed., Acad. Press, NY (1989), pp. 305-311]. Quantitative composition results at each time point were obtained by comparison to derivatized amino acid standards (1 pmol). At 0 time, contaminating glycine was detected. Alanine was the only amino acid that increased with incubation time. After 2 h incubation, Ala was detected at a total amount of 25 pmol, equivalent to 0.66 mole of Ala released per mole of protein. This result indicated that the natural mammalian SCF molecule contains Ala as its carboxyl terminus, consistent with the sequence analysis of a C-terminal peptide, S-2, which contains C-terminal Ala. This conclusion is also consistent with the known specificity of carboxypeptidase P [Lu et al., J. Chromatog. 447, 351-364 (1988)]. For example, cleavage ceases if the sequence Pro-Val is encountered. Peptide S-2 has the sequence S-R-V-S-V-(T)-K-P-F-M-L-P-P-V-A-(A) and was deduced to be the C-terminal peptide of SCF (see Section J in this Example). The C-terminal sequence of ---P-V-A-(A) restricts the protease cleavage to alanine only. The amino acid composition of peptide S-2 indicates the presence of 1 Thr, 2 Ser, 3 Pro, 2 Ala, 3 Val, 1 Met, 1 Leu, 1 Phe, 1 Lys, and 1 Arg, totalling 16 residues. The detection of 2 Ala residues indicates that there may

be two Ala residues at the C-terminus of this peptide (see table in Section G). Thus the BRL SCF terminates at Ala 164 or Ala 165.

5 J. Sequence of SCF

By combining the results obtained from sequence analysis of (1) intact stem cell factor after removing its N-terminal pyroglutamic acid, (2) the CNBr peptides, (3) the trypsin peptides, and (4) the Glu-C
10 peptidase fragments, an N-terminal sequence and a C-terminal sequence were deduced (Figure 11). The N-terminal sequence starts at pyroglutamic acid and ends at Met-48. The C-terminal sequence contains 84/85 amino
15 acids (position 82 to 164/165). The sequence from position 49 to 81 was not detected in any of the peptides isolated. However, a sequence was detected for a large peptide after BNPS-skatole cleavage of BRL SCF as described in Section H of this Example. From these
20 additional data, as well as DNA sequence obtained from rat SCF (Example 3) the N- and C-terminal sequences can be aligned and the overall sequence delineated as shown in Figure 11. The N-terminus of the molecule is pyroglutamic acid and the C-terminus is alanine as
25 confirmed by pyroglutamate aminopeptidase digestion and carboxypeptidase P digestion, respectively.

From the sequence data, it is concluded that Asn-72 is glycosylated; Asn-109 and Asn-120 are probably glycosylated in some molecules but not in others.
30 Asn-65 could be detected during sequence analysis and therefore may only be partially glycosylated, if at all. Ser-142, Thr-143 and Thr-155, predicted from DNA sequence, could not be detected during amino acid sequence analysis and therefore could be sites of
35 O-linked carbohydrate attachment. These potential carbohydrate attachment sites are indicated in

Figure 11; N-linked carbohydrate is indicated by solid bold lettering; O-linked carbohydrate is indicated by open bold lettering.

5 K. Amino Acid Compositional Analysis of BRL Stem Cell Factor

Material from the C₄ column of Figure 7 was prepared for amino acid composition analysis by
10 concentration and buffer exchange into 50 mM ammonium bicarbonate.

Two 70 µl samples were separately hydrolyzed in 6 N HCl containing 0.1% phenol and 0.05%
2-mercaptoethanol at 110°C in vacuo for 24 h. The
15 hydrolysates were dried, reconstituted into sodium citrate buffer, and analyzed using ion exchange chromatography (Beckman Model 6300 amino acid analyzer). The results are shown in Table 3. Using 164
amino acids (from the protein sequencing data) to
20 calculate amino acid composition gives a better match to predicted values than using 193 amino acids (as deduced from PCR-derived DNA sequencing data, Figure 14C).

25

30

35

Table 3

Quantitative Amino Acid Composition of Mammalian Derived SCF

5	Amino Acid	<u>Amino Acid Composition</u> <u>Moles per mole of protein</u> ¹		<u>Predicted</u> <u>Residues per molecule</u> ²	
		Run #1	Run #2	(A)	(B)
	Asx	24.46	24.26	25	28
	Thr	10.37	10.43	11	12
	Ser	14.52	14.30	16	24
	Glx	11.44	11.37	10	10
10	Pro	10.90	10.85	9	10
	Gly	5.81	6.20	4	5
	Ala	8.62	8.35	7/8	8
	Cys	nd	nd	4	5
	Val	14.03	13.96	15	15
	Met	4.05	3.99	6	7
	Ile	8.31	8.33	9	10
	Leu	17.02	16.97	16	19
15	Tyr	2.86	2.84	3	7
	Phe	7.96	7.92	8	8
	His	2.11	2.11	2	3
	Lys	10.35	11.28	12	14
	Trp	nd	nd	1	1
	Arg	4.93	4.99	5	6
20	Total	158	158	164/165	193
	Calculated molecular weight			18,424 ³	

25 1. Based on 158 residues from protein sequence analysis (excluding Cys and Trp).

2. Theoretical values calculated from protein sequence data (A) or from DNA sequence data (B).

3. Based on 1-164 sequence.

30 Inclusion of a known amount of an internal standard in the amino acid composition analyses also allowed quantitation of protein in the sample; a value of 0.117 mg/ml was obtained for the sample analyzed.

35

EXAMPLE 3

Cloning of the Genes for Rat and Human SCF

A. Amplification and Sequencing of Rat SCF cDNA

5 Fragments

Determination of the amino acid sequence of fragments of the rat SCF protein made it possible to design mixed sequence oligonucleotides specific for rat
10 SCF. The oligonucleotides were used as hybridization probes to screen rat cDNA and genomic libraries and as primers in attempts to amplify portions of the cDNA using polymerase chain reaction (PCR) strategies
15 ([Mullis et al., Methods in Enzymol. 155, 335-350 (1987)]). The oligodeoxynucleotides were synthesized by the phosphoramidite method [Beaucage, et al.,
20 Tetrahedron Lett., 22, 1859-1862 (1981); McBride, et al., Tetrahedron Lett., 24, 245-248 (1983)]; their sequences are depicted in Figure 12A. The letters represent A, adenine; T, thymine, C, cytosine;
G, guanine; I, inosine. The * in Figure 12A represents oligonucleotides which contain restriction endonuclease recognition sequences. The sequences are written 5'-3'.

A rat genomic library, a rat liver cDNA
25 library, and two BRL cDNA libraries were screened using ³²P-labelled mixed oligonucleotide probes, 219-21 and 219-22 (Figure 12A), whose sequences were based on amino acid sequence obtained as in Example 2. No SCF clones were isolated in these experiments using standard
30 methods of cDNA cloning [Maniatis, et al., Molecular Cloning, Cold Spring Harbor 212-246 (1982)].

An alternate approach which did result in the isolation of SCF nucleic acid sequences involved the use of PCR techniques. In this methodology, the region of
35 DNA encompassed by two DNA primers is amplified selectively in vitro by multiple cycles of replication

catalysed by a suitable DNA polymerase (such as TaqI DNA polymerase) in the presence of deoxynucleoside triphosphates in a thermo cycler. The specificity of PCR amplification is based on two oligonucleotide primers which flank the DNA segment to be amplified and hybridize to opposite strands. PCR with double-sided specificity for a particular DNA region in a complex mixture is accomplished by use of two primers with sequences sufficiently specific to that region. PCR with single-sided specificity utilizes one region-specific primer and a second primer which can prime at target sites present on many or all of the DNA molecules in a particular mixture [Loh et al., Science, 243, 217-220 (1989)].

The DNA products of successful PCR amplification reactions are sources of DNA sequence information [Gyllensten, Biotechniques, 7, 700-708 (1989)] and can be used to make labeled hybridization probes possessing greater length and higher specificity than oligonucleotide probes. PCR products can also be designed, with appropriate primer sequences, to be cloned into plasmid vectors which allow the expression of the encoded peptide product.

The basic strategy for obtaining the DNA sequence of the rat SCF cDNA is outlined in Figure 13A. The small arrows indicate PCR amplifications and the thick arrows indicate DNA sequencing reactions. PCRs 90.6 and 96.2, in conjunction with DNA sequencing, were used to obtain partial nucleic acid sequence for the rat SCF cDNA. The primers used in these PCRs were mixed oligonucleotides based on amino acid sequence depicted in Figure 11. Using the sequence information obtained from PCRs 90.6 and 96.2, unique sequence primers (224-27 and 224-28, Figure 12A) were made and used in subsequent amplifications and sequencing reactions. DNA containing

the 5' end of the cDNA was obtained in PCRs 90.3, 96.6, and 625.1 using single-sided specificity PCR.

Additional DNA sequence near the C-terminus of SCF protein was obtained in PCR 90.4. DNA sequence for the remainder of the coding region of rat SCF cDNA was obtained from PCR products 630.1, 630.2, 84.1 and 84.2 as described below in section C of this Example. The techniques used in obtaining the rat SCF cDNA are described below.

RNA was prepared from BRL cells as described by Okayama et al. [Methods Enzymol., 154, 3-28 (1987)]. PolyA+ RNA was isolated using an oligo(dT) cellulose column as described by Jacobson in [Methods in Enzymology, volume 152, 254-261 (1987)].

First-strand cDNA was synthesized using 1 µg of BRL polyA+ RNA as template and (dT)₁₂₋₁₈ as primer according to the protocol supplied with the enzyme, Mo-MLV reverse transcriptase (Bethesda Research Laboratories). RNA strand degradation was performed using 0.14 M NaOH at 84°C for 10 min or incubation in a boiling water bath for 5 min. Excess ammonium acetate was added to neutralize the solution, and the cDNA was first extracted with phenol/chloroform, then extracted with chloroform/iso-amyl alcohol, and precipitated with ethanol. To make possible the use of oligo(dC)-related primers in PCRs with single-sided specificity, a poly(dG) tail was added to the 3' terminus of an aliquot of the first-strand cDNA with terminal transferase from calf thymus (Boeringer Mannheim) as previously described [Deng et al., Methods Enzymol., 100, 96-103 (1983)].

Unless otherwise noted in the descriptions which follow, the denaturation step in each PCR cycle was set at 94°C, 1 min; and elongation was at 72°C for 3 or 4 min. The temperature and duration of annealing was variable from PCR to PCR, often representing a compromise based on the estimated requirements of

several different PCRs being carried out simultaneously. When primer concentrations were reduced to lessen the accumulation of primer artifacts [Watson, Amplifications, 2, 56 (1989)], longer annealing times
5 were indicated; when PCR product concentration was high, shorter annealing times and higher primer concentrations were used to increase yield. A major factor in determining the annealing temperature was the estimated T_d of primer-target association [Suggs et al., in
10 Developmental Biology Using Purified Genes eds. Brown, D.D. and Fox, C.F. (Academic, New York) pp. 683-693 (1981)]. The enzymes used in the amplifications were obtained from either of three
15 manufacturers: Stratagene, Promega, or Perkin-Elmer Cetus. The reaction compounds were used as suggested by the manufacturer. The amplifications were performed in either a Coy Tempcycle or a Perkin-Elmer Cetus DNA thermocycler.

Amplification of SCF cDNA fragments was
20 usually assayed by agarose gel electrophoresis in the presence of ethidium bromide and visualization by fluorescence of DNA bands stimulated by ultraviolet irradiation. In some cases where small fragments were anticipated, PCR products were analyzed by
25 polyacrylamide gel electrophoresis. Confirmation that the observed bands represented SCF cDNA fragments was obtained by observation of appropriate DNA bands upon subsequent amplification with one or more internally-nested primers. Final confirmation was by dideoxy
30 sequencing [Sanger et al., Proc. Natl. Acad. Sci. USA, 74, 5463-5467 (1977)] of the PCR product and comparison of the predicted translation products with SCF peptide sequence information.

In the initial PCR experiments, mixed
35 oligonucleotides based on SCF protein sequence were used [Gould, Proc. Natl. Acad. Sci. USA, 86, 1934-1938

(1989)]. Below are descriptions of the PCR amplifications that were used to obtain DNA sequence information for the rat cDNA encoding amino acids -25 to 162.

- 5 In PCR 90.6, BRL cDNA was amplified with
4 pmol each of 222-11 and 223-6 in a reaction volume of
20 μ l. An aliquot of the product of PCR 90.6 was
electrophoresed on an agarose gel and a band of about
the expected size was observed. One μ l of the PCR 90.6
10 product was amplified further with 20 pmol each of
primers 222-11 and 223-6 in 50 μ l for 15 cycles,
annealing at 45°C. A portion of this product was then
subjected to 25 cycles of amplification in the presence \Rightarrow
of primers 222-11 and 219-25 (PCR 96.2), yielding a
15 single major product band upon agarose gel
electrophoresis. Asymmetric amplification of the
product of PCR 96.2 with the same two primers produced a
template which was successfully sequenced. Further
selective amplification of SCF sequences in the product
20 of 96.2 was performed by PCR amplification of the
product in the presence of 222-11 and nested primer
219-21. The product of this PCR was used as a template
for asymmetric amplification and radiolabelled probe
production (PCR2).
- 25 To isolate the 5' end of the rat SCF cDNA,
primers containing (dC)_n sequences, complimentary to the
poly(dG) tails of the cDNA, were utilized as non-
specific primers. PCR 90.3 contained (dC)₁₂ (10 pmol)
and 223-6 (4 pmol) as primers and BRL cDNA as
30 template. The reaction product acted like a very high
molecular weight aggregate, remaining close to the
loading well in agarose gel electrophoresis. One μ l of
the product solution was further amplified in the
presence of 25 pmol of (dC)₁₂ and 10 pmol 223-6 in a
35 volume of 25 μ l for 15 cycles, annealing at 45°C. One-
half μ l of this product was then amplified for 25 cycles

with internally nested primer 219-25 and 201-7 (PCR 96.6). The sequence of 201-7 is shown in Figure 12C. No bands were observed by agarose gel electrophoresis. Another 25 cycles of PCR, annealing at 40°C, were performed, after which one prominent band was observed. Southern blotting was carried out and a single prominent hybridizing band was observed. An additional 20 cycles of PCR (625.1), annealing at 45°C, were performed using 201-7 and nested primer 224-27. Sequencing was performed after asymmetric amplification by PCR, yielding sequence which extended past the putative amino terminus of the presumed signal peptide coding sequence of pre-SCF. This sequence was used to design oligonucleotide primer 227-29 containing the 5' end of the coding region of the rat SCF cDNA. Similarly, the 3' DNA sequence ending at amino acid 162 was obtained by sequencing PCR 90.4 (see Figure 13.A).

The sequence of the rat SCF coding region downstream of codon 162 was obtained by direct sequencing of the products of PCRs in which rat SCF (+)-strand primers were combined with (-)-strand primers designed from the human SCF 3'-untranslated region sequence. Rat SCF primers 224-24 (Figure 12A) or 227-31 (5'-CCTGAGAAAGATTCCAGAGTC-3') were used in combination with either of the two human SCF primers 283-19 (5'-CTGCAGTTTGTATCTGAAG-3') or 283-20 (5'-CATATAAAGTCATGGGTAG-3'). The rat SCF cDNA sequence is shown in Figure 14C.

B. Cloning of the Rat Stem Cell Factor Genomic DNA

Probes made from PCR amplification of cDNA encoding rat SCF as described in section A above were used to screen a library containing rat genomic sequences (obtained from CLONTECH Laboratories, Inc.; catalog number RL1022 j). The library was constructed

in the bacteriophage λ vector EMBL-3 SP6/T7 using DNA obtained from an adult male Sprague-Dawley rat. The library, as characterized by the supplier, contains 2.3×10^6 independent clones with an average insert size of 16 kb.

PCRs were used to generate ^{32}P -labeled probes used in screening the genomic library. Probe PCR1 (Figure 13A) was prepared in a reaction which contained 16.7 μM ^{32}P [α]-dATP, 200 μM dCTP, 200 μM dGTP, 200 μM dTTP, reaction buffer supplied by Perkin Elmer Cetus, Taq polymerase (Perkin Elmer Cetus) at 0.05 units/ml, 0.5 μM 219-26, 0.05 μM 223-6 and 1 μl of template 90.1 containing the target sites for the two primers. Probe PCR 2 was made using similar reaction conditions except that the primers and template were changed. Probe PCR 2 was made using 0.5 μM 222-11, 0.05 μM 219-21 and 1 μl of a template derived from PCR 96.2.

Approximately 10^6 bacteriophage were plated as described in Maniatis et al. [supra (1982)]. The plaques were transferred to GeneScreen Plus[™] filters (22cm x 22cm; NEN/DuPont) which were denatured, neutralized and dried as described in a protocol from the manufacturer. Two filter transfers were performed for each plate.

The filters were prehybridized in 1M NaCl, 1% SDS, 0.1% bovine serum albumin, 0.1% ficoll, 0.1% polyvinylpyrrolidone (hybridization solution) for approximately 16 h at 65°C and stored at -20°C. The filters were transferred to fresh hybridization solution containing ^{32}P -labeled PCR 1 probe at 1.2×10^5 cpm/ml and hybridized for 14 h at 65°C. The filters were washed in 0.9 M NaCl, 0.09 M sodium citrate, 0.1% SDS, pH 7.2 (wash solution) for 2 h at room temperature followed by a second wash in fresh wash solution for 30 min at 65°C. Bacteriophage clones from the areas of

the plates corresponding to radioactive spots on autoradiograms were removed from the plates and rescreened with probes PCR1 and PCR2.

DNA from positive clones was digested with
5 restriction endonucleases BamHI, SphI or SstI, and the
resulting fragments were subcloned into pUC119 and
subsequently sequenced. The strategy for sequencing the
rat genomic SCF DNA is shown schematically in
10 Figure 14A. In this figure, the line drawing at the top
represents the region of rat genomic DNA encoding SCF.
The gaps in the line indicate regions that have not been
sequenced. The large boxes represent exons for coding
regions of the SCF gene with the corresponding encoded
amino acids indicated above each box. The arrows
15 represent the individual regions that were sequenced and
used to assemble the consensus sequence for the rat SCF
gene. The sequence for rat SCF gene is shown in
Figure 14B.

Using PCR 1 probe to screen the rat genomic
20 library, clones corresponding to exons encoding amino
acids 19 to 176 of SCF were isolated. To obtain clones
for exons upstream of the coding region for amino acid
19, the library was screened using oligonucleotide probe
228-30. The same set of filters used previously with
25 probe PCR 1 were prehybridized as before and hybridized
in hybridization solution containing ^{32}P -labeled
oligonucleotide 228-30 (0.03 picomole/ml) at 50°C for
16 h. The filters were washed in wash solution at room
temperature for 30 min followed by a second wash in
30 fresh wash solution at 45°C for 15 min. Bacteriophage
clones from the areas of the plates corresponding to
radioactive spots on autoradiograms were removed from
the plates and rescreened with probe 228-30. DNA from
positive clones was digested with restriction
35 endonucleases and subcloned as before. Using probe
228-30, clones corresponding to the exon encoding amino
acids -20 to 18 were obtained.

Several attempts were made to isolate clones corresponding to the exon(s) containing the 5'-untranslated region and the coding region for amino acids -25 to -21. No clones for this region of the rat SCF gene have been isolated.

C. Cloning Rat cDNA for Expression in Mammalian Cells

Mammalian cell expression systems were devised to ascertain whether an active polypeptide product of rat SCF could be expressed in and secreted by mammalian cells. Expression systems were designed to express truncated versions of rat SCF (SCF¹⁻¹⁶² and SCF¹⁻¹⁶⁴) and a protein (SCF¹⁻¹⁹³) predicted from the translation of the gene sequence in Fig. 14C.

The expression vector used in these studies was a shuttle vector containing pUC119, SV40 and HTLVII sequences. The vector was designed to allow autonomous replication in both E. coli and mammalian cells and to express inserted exogenous DNA under the control of viral DNA sequences. This vector, designated V19.8, harbored in E. coli DH5, is deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Md. (ATCC# 68124). This vector is a derivative of pSVDM19 described in Souza U.S. Patent 4,810,643 hereby incorporated by reference.

The cDNA for rat SCF¹⁻¹⁶² was inserted into plasmid vector V19.8. The cDNA sequence is shown in Figure 14C. The cDNA that was used in this construction was synthesized in PCR reactions 630.1 and 630.2, as shown in Figure 13A. These PCRs represent independent amplifications and utilized synthetic oligonucleotide primers 227-29 and 227-30. The sequence for these primers was obtained from PCR generated cDNA as described in section A of this Example. The reactions, 50 µl in volume, consisted of 1x reaction buffer (from a

Perkin Elmer Cetus kit), 250 μ M dATP, 250 μ M dCTP, 250 μ M dGTP, and 250 μ M dTTP, 200 ng oligo(dT)-primed cDNA, 1 picomole of 227-29, 1 picomole of 227-30, and 2.5 units of Taq polymerase (Perkin Elmer Cetus). The cDNA was amplified for 10 cycles using a denaturation temperature of 94°C for 1 min, an annealing temperature of 37°C for 2 min, and an elongation temperature of 72°C for 1 min. After these initial rounds of PCR amplification, 10 picomoles of 227-29 and 10 picomoles of 227-30 were added to each reaction. Amplifications were continued for 30 cycles under the same conditions with the exception that the annealing temperature was changed to 55°C. The products of the PCR were digested with restriction endonucleases HindIII and SstII. V19.8 was similarly digested with HindIII and SstII, and in one instance, the digested plasmid vector was treated with calf intestinal alkaline phosphatase; in other instances, the large fragment from the digestion was isolated from an agarose gel. The cDNA was ligated to V19.8 using T4 polynucleotide ligase. The ligation products were transformed into competent *E. coli* strain DH5 as described [Okayama, et. al., supra (1987)]. DNA prepared from individual bacterial clones was sequenced by the Sanger dideoxy method. Figure 17 shows a construct of V19.8 SCF. These plasmids were used to transfect mammalian cells as described in Example 4 and Example 5.

The expression vector for rat SCF¹⁻¹⁶⁴ was constructed using a strategy similar to that used for SCF¹⁻¹⁶² in which cDNA was synthesized using PCR amplification and subsequently inserted into V19.8. The cDNA used in the constructions was synthesized in PCR amplifications with V19.8 containing SCF¹⁻¹⁶² cDNA (V19.8:SCF¹⁻¹⁶²) as template, 227-29 as the primer for the 5'-end of the gene and 237-19 as the primer for the 3'-end of the gene. Duplicate reactions (50 μ l)

contained 1x reaction buffer, 250 μ M each of dATP, dCTP, dGTP and dTTP, 2.5 units of Taq polymerase, 20 ng of V19.8:SCF¹⁻¹⁶², and 20 picomoles of each primer. The cDNA was amplified for 35 cycles using a denaturation temperature of 94°C for 1 min, an annealing temperature of 55°C for 2 min and an elongation temperature of 72°C for 2 min. The products of the amplifications were digested with restriction endonucleases HindIII and SstII and inserted into V19.8. The resulting vector contains the coding region for amino acids -25 to 164 of SCF followed by a termination codon.

The cDNA for a 193 amino acid form of rat SCF, (rat SCF¹⁻¹⁹³) is predicted from the translation of the DNA sequence in Figure 14C) was also inserted into plasmid vector V19.8 using a protocol similar to that used for the rat SCF¹⁻¹⁶². The cDNA that was used in this construction was synthesized in PCR reactions 84.1 and 84.2 (Figure 13A) utilizing oligonucleotides 227-29 and 230-25. The two reactions represent independent amplifications starting from different RNA preparations. The sequence for 227-29 was obtained via PCR reactions as described in section A of this Example and the sequence for primer 230-25 was obtained from rat genomic DNA (Figure 14B). The reactions, 50 μ l in volume, consisted of 1x reaction buffer (from a Perkin Elmer Cetus kit), 250 μ M dATP, 250 μ M dCTP, 250 μ M dGTP, and 250 μ M dTTP, 200 ng oligo(dT)-primed cDNA, 10 picomoles of 227-29, 10 picomoles of 230-25, and 2.5 units of Taq polymerase (Perkin Elmer Cetus). The cDNA was amplified for 5 cycles using a denaturation temperature of 94°C for 1 1/2 minutes, an annealing temperature of 50°C for 2 min, and an elongation temperature of 72°C for 2 min. After these initial rounds, the amplifications were continued for 35 cycles under the same conditions with the exception that the annealing temperature was changed to 60°C. The products

of the PCR amplification were digested with restriction endonucleases HindIII and SstII. V19.8 DNA was digested with HindIII and SstII and the large fragment from the digestion was isolated from an agarose gel. The cDNA
5 was ligated to V19.8 using T4 polynucleotide ligase. The ligation products were transformed into competent E. coli strain DH5 and DNA prepared from individual bacterial clones was sequenced. These plasmids were used to transfect mammalian cells in Example 4.

10

D. Amplification and Sequencing of Human SCF cDNA
PCR Products

The human SCF cDNA was obtained from a
15 hepatoma cell line HepG2 (ATCC HB 8065) using PCR amplification as outlined in Figure 13B. The basic strategy was to amplify human cDNA by PCR with primers whose sequence was obtained from the rat SCF cDNA.

RNA was prepared as described by Maniatis
20 et al. [supra (1982)]. PolyA⁺ RNA was prepared using oligo dT cellulose following manufacturers directions. (Collaborative Research Inc.).

First strand cDNA was prepared as described above for BRL cDNA, except that synthesis was primed
25 with 2 μ M oligonucleotide 228-28, shown in Figure 12C, which contains a short random sequence at the 3' end attached to a longer unique sequence. The unique-sequence portion of 228-28 provides a target site for amplification by PCR with primer 228-29 as non-specific
30 primer. Human cDNA sequences related to at least part of the rat SCF sequence were amplified from the HepG2 cDNA by PCR using primers 227-29 and 228-29 (PCR 22.7, see Figure 13B; 15 cycles annealing at 60°C followed by 15 cycles annealing at 55°C). Agarose gel
35 electrophoresis revealed no distinct bands, only a smear of apparently heterogeneously sized DNA. Further

preferential amplification of sequences closely related to rat SCF cDNA was attempted by carrying out PCR with 1 μ l of the PCR 22.7 product using internally nested rat SCF primer 222-11 and primer 228-29 (PCR 24.3; 20 cycles annealing at 55°C). Again only a heterogeneous smear of DNA product was observed on agarose gels. Double-sided specific amplification of the PCR 24.3 products with primers 222-11 and 227-30 (PCR 25.10; 20 cycles) gave rise to a single major product band of the same size as the corresponding rat SCF cDNA PCR product. Sequencing of an asymmetric PCR product (PCR 33.1) DNA using 224-24 as sequencing primer yielded about 70 bases of human SCF sequences.

Similarly, amplification of 1 μ l of the PCR 22.7 product, first with primers 224-25 and 228-29 (PCR 24.7, 20 cycles), then with primers 224-25 and 227-30 (PCR 41.11) generated one major band of the same size as the corresponding rat SCF product, and after asymmetric amplification (PCR 42.3) yielded a sequence which was highly homologous to the rat SCF sequence when 224-24 was used as sequencing primer. Unique sequence oligodeoxynucleotides targeted at the human SCF cDNA were synthesized and their sequences are given in Figure 12B.

To obtain the human counterpart of the rat SCF PCR-generated coding sequence which was used in expression and activity studies, a PCR with primers 227-29 and 227-30 was performed on 1 μ l of PCR 22.7 product in a reaction volume of 50 μ l (PCR 39.1). Amplification was performed in a Coy Tempcycler. Because the degree of mismatching between the human SCF cDNA and the rat SCF unique primer 227-30 was unknown, a low stringency of annealing (37°C) was used for the first three cycles; afterward annealing was at 55°C. A prominent band of the same size (about 590 bp) as the rat homologue appeared, and was further amplified by

dilution of a small portion of PCR 39.1 product and PCR with the same primers (PCR 41.1). Because more than one band was observed in the products of PCR 41.1, further PCR with nested internal primers was performed in order to determine at least a portion of its sequence before cloning. After 23 cycles of PCR with primers 231-27 and 227-29 (PCR 51.2), a single, intense band was apparent. Asymmetric PCRs with primers 227-29 and 231-27 and sequencing confirmed the presence of the human SCF cDNA sequences. Cloning of the PCR 41.1 SCF DNA into the expression vector V19.8 was performed as already described for the rat SCF 1-162 PCR fragments in Section C above. DNA from individual bacterial clones was sequenced by the Sanger dideoxy method.

15

E. Cloning of the Human Stem Cell Factor Genomic DNA

A PCR7 probe made from PCR amplification of cDNA, see Figure 13B, was used to screen a library containing human genomic sequences. A riboprobe complementary to a portion of human SCF cDNA, see below, was used to re-screen positive plaques. PCR 7 probe was prepared starting with the product of PCR 41.1 (see Figure 13B). The product of PCR 41.1 was further amplified with primers 227-29 and 227-30. The resulting 590 bp fragment was eluted from an agarose gel and reamplified with the same primers (PCR 58.1). The product of PCR 58.1 was diluted 1000-fold in a 50 μ l reaction containing 10 pmoles 233-13 and amplified for 10 cycles. After the addition of 10 pmoles of 227-30 to the reaction, the PCR was continued for 20 cycles. An additional 80 pmoles of 233-13 was added and the reaction volume increased to 90 μ l and the PCR was continued for 15 cycles. The reaction products were diluted 200-fold in a 50 μ l reaction, 20 pmoles of 231-27 and 20 pmoles of 233-13 were added, and PCR was

performed for 35 cycles using an annealing temperature of 48° in reaction 96.1. To produce ³²P-labeled PCR7, reaction conditions similar to those used to make PCR1 were used with the following exceptions: in a reaction
5 volume of 50 µl, PCR 96.1 was diluted 100-fold; 5 pmoles of 231-27 was used as the sole primer; and 45 cycles of PCR were performed with denaturation at 94° for 1 minute, annealing at 48° for 2 minutes and elongation at 72° for 2 minutes.

10 The riboprobe, riboprobe 1, was a ³²P-labelled single-stranded RNA complementary to nucleotides 2-436 of the hSCF DNA sequence shown in Figure 15B. To construct the vector for the production of this probe, PCR 41.1 (Figure 13B) product DNA was digested with
15 HindIII and EcoRI and cloned into the polylinker of the plasmid vector pGEM3 (Promega, Madison, Wisconsin). The recombinant pGEM3:hSCF plasmid DNA was then linearized by digestion with HindIII. ³²P-labeled riboprobe 1 was prepared from the linearized plasmid DNA by runoff
20 transcription with T7 RNA polymerase according to the instructions provided by Promega. The reaction (3 µl) contained 250 ng of linearized plasmid DNA and 20 µM ³²P-rCTP (catalog #NEG-008H, New England Nuclear (NEN) with no additional unlabeled CTP.

25 The human genomic library was obtained from Stratagene (La Jolla, CA; catalog #:946203). The library was constructed in the bacteriophage Lambda Fix II vector using DNA prepared from a Caucasian male placenta. The library, as characterized by the
30 supplier, contained 2x10⁶ primary plaques with an average insert size greater than 15 kb. Approximately 10⁶ bacteriophage were plated as described in Maniatis, et al. [supra (1982)]. The plaques were transferred to Gene Screen Plus™ filters (22 cm²; NEN/DuPont) according
35 to the protocol from the manufacturer. Two filter transfers were performed for each plate.

The filters were prehybridized in 6XSSC (0.9 M NaCl, 0.09 M sodium citrate pH 7.5), 1% SDS at 60°C. The filters were hybridized in fresh 6XSSC, 1% SDS solution containing ^{32}P -labeled PCR 7 probe at 2×10^5 cpm/ml and hybridized for 20 h at 62°C. The filters were washed in 6XSSC, 1% SDS for 16 h at 62°C. A bacteriophage plug was removed from an area of a plate which corresponded to radioactive spots on autoradiograms and rescreened with probe PCR 7 and riboprobe 1. The rescreen with PCR 7 probe was performed using conditions similar to those used in the initial screen. The rescreen with riboprobe 1 was performed as follows: the filters were prehybridized in 6XSSC, 1% SDS and hybridized at 62°C for 18 h in 0.25 M NaPO_4 , (pH 7.5), 0.25 M NaCl, 0.001 M EDTA, 15% formamide, 7% SDS and riboprobe at 1×10^6 cpm/ml. The filters were washed in 6XSSC, 1% SDS for 30 min at 62°C followed by 1XSSC, 1% SDS for 30 min at 62°C. DNA from positive clones was digested with restriction endonucleases Bam HI, SphI or SstI and the resulting fragments were subcloned into pUC119 and subsequently sequenced.

Using probe PCR 7, a clone was obtained that included exons encoding amino acids 40 to 176 and this clone is deposited at the ATCC (deposit #40681). To obtain clones for additional SCF exons, the human genomic library was screened with riboprobe 2 and oligonucleotide probe 235-29. The library was screened in a manner similar to that done previously with the following exceptions: the hybridization with probe 235-29 was done at 37°C and the washes for this hybridization were for 1 h at 37°C and 1 h at 44°C. Positive clones were rescreened with riboprobe 2, riboprobe 3 and oligonucleotide probes 235-29 and 236-31. Riboprobes 2 and 3 were made using a protocol similar to that used to produce riboprobe 1, with the

following exceptions: (a) the recombinant pGEM3:hSCF
plasmid DNA was linearized with restriction endonuclease
PvuII (riboprobe 2) or PstI (riboprobe 3) and (b) the
SP6 RNA polymerase (Promega) was used to synthesize
5 riboprobe 3.

Figure 15A shows the strategy used to sequence
human genomic DNA. In this figure, the line drawing at
the top represents the region of human genomic DNA
encoding SCF. The gaps in the line indicate regions
10 that have not been sequenced. The large boxes represent
exons for coding regions of the SCF gene with the
corresponding encoded amino acids indicated above each
box. The sequence of the human SCF gene is shown in
Figure 15B. The sequence of human SCF cDNA obtained PCR
15 techniques is shown in Figure 15C.

The sequence of exons 7, 8 and 9, which
include the coding region for amino acids 177 to 248,
were obtained from a bacteriophage lambda clone isolated
as described above using PCR7 as probe.

20 To isolate a clone of exon 1 of the human SCF
gene, a second genomic library was screened. The
library, purchased from Clontech (Palo Alto, CA; catalog
#HL 1067 J), was constructed in bacteriophage lambda
vector EMBL3 SP6/T7 and contained 2.5×10^6 independent
25 clones with an average insert size of 15 kb.
Approximately 10^6 clones were plated and screened as
described above using oligonucleotide probe 249-31
(5'-ACTTGTGTCTTCTTCATAAGGAAAGGC-3). A SacI restriction
fragment of the lambda clone was cloned into plasmid
30 vector pGEM4 for subsequent sequence analysis. The
sequence of the human SCF gene including exons 1, 7, 8
and 9 is shown in Figure 15D.

- F. Sequence of the Human SCF cDNA 5' Region

35

Sequencing of products from PCRs primed by two
gene-specific primers reveals the sequence of the region

bounded by the 3' ends of the two primers. One-sided
PCRs, as indicated in Example 3A, can yield the sequence
of flanking regions. One-sided PCR was used to extend
the sequence of the 5'-untranslated region of human SCF
5 cDNA.

First strand cDNA was prepared from poly A+
RNA from the human bladder carcinoma cell line 5637
(ATCC HTB 9) using oligonucleotide 228-28 (Figure 12C)
as primer, as described in Example 3D. Tailing of this
10 cDNA with dG residues, followed by one-sided PCR
amplification using primers containing (dC)_n sequences
in combination with SCF-specific primers, failed to
yield cDNA fragments extending upstream (5') of the
known sequence.

15 A small amount of sequence information was
obtained from PCR amplification of products of second
strand synthesis primed by oligonucleotide 228-28. The
untailed 5637 first strand cDNA described above (about
50 ng) and 2 pmol of 228-28 were incubated with Klenow
20 polymerase and 0.5 mM each of dATP, dCTP, dGTP and dTTP
at 10-12°C for 30 minutes in 10 uL of 1xNick-translation
buffer [Maniatis et al., Molecular Cloning, a Laboratory
Manual, Cold Spring Harbor Laboratory (1982)].
Amplification of the resulting cDNA by sequential one-
25 sided PCRs with primer 228-29 in combination with nested
SCF primers (in order of use: 235-30, 233-14, 236-31
and finally 235-29) yielded complex product mixtures
which appeared as smears on agarose gels. Significant
enrichment of SCF-related cDNA fragments was indicated
30 by the increasing intensity of the specific product band
observed when comparable volumes of the successive one-
sided PCR products were amplified with two SCF primers
(227-29 and 235-29, for example, yielding a product of
about 150 bp). Attempts to select for a particular size
35 range of products by punching out portions of the
agarose gel smears and reamplifying by PCR in most cases

failed to yield a well-defined band which contained SCF-related sequences.

One reaction, PCR 16.17, which contained only the 235-29 primer, gave rise to a band which apparently
5 arose from priming by 235-29 at an unknown site 5' of the coding region in addition to the expected site, as shown by mapping with the restriction enzymes PvuII and PstI and PCR analysis with nested primers. This product was gel-purified and reamplified with primer 235-29, and
10 sequencing was attempted by the Sanger dideoxy method using ^{32}P -labelled primer 228-30. The resulting sequence was the basis for the design of oligonucleotide 254-9 (Figure 12B). When this 3' directed primer was
15 used in subsequent PCRs in combination with 5' directed SCF primers, bands of the expected size were obtained. Direct Sanger sequencing of such PCR products yielded nucleotides 180 through 204 of a human SCF cDNA sequence, Figure 15C.

In order to obtain more sequence at the 5' end
20 of the hSCF cDNA, first strand cDNA was prepared from 5637 poly A⁺ RNA (about 300 ng) using an SCF-specific primer (2 pmol of 233-14) in a 16 uL reaction containing 0.2 U MMLV reverse transcriptase (purchased from BRL) and 500 uM each dNTP. After standard phenol-chloroform
25 and chloroform extractions and ethanol precipitation (from 1 M ammonium acetate) steps, the nucleic acids were resuspended in 20 uL of water, placed in a boiling water bath for 5 minutes, then cooled and tailed with terminal transferase in the presence of 8 uM dATP in a
30 CoCl_2 -containing buffer [Deng and Wu, Methods in Enzymology, 100, pp. 96-103]. The product, (dA)_n-tailed first-strand cDNA was purified by phenol-chloroform extraction and ethanol precipitation and resuspended in 20 uL of 10mM tris, pH 8.0, and 1mM EDTA.

35 Enrichment and amplification of human SCF-related cDNA 5' end fragments from about 20 ng of the

(dA)_n-tailed 5637 cDNA was performed as follows: an initial 26 cycles of one-sided PCR were performed in the presence of SCF-specific primer 236-31 and a primer or primer mixture containing (dT)_n sequences at or near the 3' end, for instance primer 221-12 or a mixture of primers 220-3, 220-7, and 220-11 (Figure 12C). The products (1 μ l) of these PCRs were then amplified in a second set of PCRs containing primers 221-12 and 235-29. A major product band of approximately 370 bp was observed in each case upon agarose gel analysis. A gel plug containing part of this band was punched out of the gel with the tip of a Pasteur pipette and transferred to a small microfuge tube. 10 μ L of water was added and the plug was melted in an 84°C heating block. A PCR containing primers 221-12 and 235-29 (8 pmol each) in 40 μ L was inoculated with 2 μ L of the melted, diluted gel plug. After 15 cycles, a slightly diffuse band of approximately 370 bp was visible upon agarose gel analysis. Asymmetric PCRs were performed to generate top and bottom strand sequencing templates: for each reaction, 4 μ L of PCR reaction product and 40 pmol of either primer 221-12 or primer 235-29 in a total reaction volume of 100 μ L were subjected to 25 cycles of PCR (1 minute, 95°C; 30 seconds, 55°C; 40 seconds, 72°C). Direct sequencing of the 221-12 primed PCR product mixtures (after the standard extractions and ethanol precipitation) with ³²P-labelled primer 262-13 (Figure 12B) yielded the 5' sequence from nucleotide 1 to 179 (Figure 15C).

G. Amplification and Sequencing of Human Genomic DNA at the Site of the First Coding Exon of the Stem Cell Factor

Screening of a human genomic library with SCF oligonucleotide probes failed to reveal any clones

containing the known portion of the first coding exon. An attempt was then initiated to use a one-sided PCR technique to amplify and clone genomic sequences surrounding this exon.

5 Primer extension of heat-denatured human
placental DNA (purchased from Sigma) was performed with
DNA polymerase I (Klenow enzyme, large fragment;
Boehringer-Mannheim) using a non-SCF primer such as
228-28 or 221-11 under non-stringent (low temperature)
10 conditions, such as 12°C, to favor priming at a very
large number of different sites. Each reaction was then
diluted five-fold into TaqI DNA polymerase buffer
containing TaqI polymerase and 100 uM of each dNTP, and =
elongation of DNA strands was allowed to proceed at 72°C -
15 for 10 minutes. The product was then enriched for stem
cell factor first exon sequences by PCR in the presence
of an SCF first exon oligonucleotide (such as 254-9) and
the appropriate non-SCF primer (228-29 or 221-11).
Agarose gel electrophoresis revealed that most of the
20 products were short (less than 300 bp). To enrich for
longer species, the portion of each agarose gel lane
corresponding to length greater than 300 bp was cut out
and electrophoretically eluted. After ethanol
precipitation and resuspension in water, the gel purified
25 PCR products were cloned into a derivative of pGEM4
containing an SfiI site as a HindIII to SfiI fragment.

Colonies were screened with a ³²P-labelled SCF
first exon oligonucleotide. Several positive colonies
were identified and the sequences of the inserts were
30 obtained by the Sanger method. The resulting sequence,
which extends downstream from the first exon through a
consensus exon-intron boundary into the neighboring
intron, is shown in Figure 15B.

H. Amplification and Sequencing of SCF
cDNA Coding Regions from Mouse, Monkey, Dog, Cat, Cow
and Chicken

5 First strand cDNA was prepared from total RNA
or poly A⁺ RNA from monkey liver (purchased from
Clontech) and from the cell lines NIH-3T3 (mouse, ATCC
CRL 1658), D17 (dog, ATCC CCL 183), bovine endothelial
10 cell line (provided by Yves DeClerck, Childrens Hospital
Los Angeles, Los Angeles, California), feline embryonic
fibroblast cell line (Jarrett et al., J. Gen. Virology,
20:169-175 (1973)) and chicken brain RNA. The primer
used in first strand cDNA synthesis was either the
nonspecific primer 228-28 or an SCF primer (227-30,
15 237-19, 237-20, 230-25 or 241-6).

PCR amplification with primer 227-29 and one
of the primers 227-30, 237-19 or 237-20 in each case
except chicken yielded a fragment of the expected size
which was sequenced either directly or after cloning
20 into V19.8 or a pGEM vector. Additional sequences near
the 5' end of the SCF cDNAs were obtained from PCR
amplifications utilizing an SCF-specific primer in
combination with either 254-9 or one of the non-specific
primers 228-29 and 221-11. Additional sequences at the
25 3' end of the SCF coding regions were obtained after PCR
amplification of 228-28 primed cDNA with combinations of
SCF coding region (+)-strand primers with (-)-primers
based on the human SCF 3' untranslated region as
described in Example 3A. The primers 283-19 and 283-20
30 (Example 3A) and primer 287-9
(5'-TGTACGAAAGTAACAGTGTG-3') were used. In the case of
chicken, amplification was accomplished with primers to
227-29 or 247-1 (5'-ACTGCTCCTATTTAATCCTCTC-3') in
combination with 247-2 (5'-CACTGACTCTGGAATCTTTCTCA-3')
35 or 287-9. The aligned amino acid sequences of human
(Figure 42), monkey, dog, mouse, rat, cat, cow and
chicken. SCF mature proteins are shown in Figure 16.

The known SCF amino acid sequences are highly homologous throughout much of their length. Identical consensus signal peptide sequences are present in the coding regions of all seven species. The amino acid
5 expected to be at the amino terminus of the mature protein by analogy with the rat SCF is designated by the numeral 1 in this figure. The dog and cow cDNA sequence contains an ambiguity which results in a valine/leucine ambiguity in the amino acid sequence at codon 129. The
10 human, monkey, rat and mouse amino acid sequences co-align without any insertions or deletions. The dog sequence has a single extra residue at position 130 as compared to the other species. Human and monkey differ
15 at only one position, a conservative replacement of valine (human) by alanine (monkey) at position 130. The predicted SCF sequence immediately before and after the putative processing site near residue 164, is highly conserved between species.

EXAMPLE 4

Expression of Recombinant Rat SCF in COS-1 Cells

For transient expression in COS-1 cells (ATCC CRL 1650), vector V19.8 (Example 3C) containing the rat
25 SCF¹⁻¹⁶² and SCF¹⁻¹⁹³ genes was transfected into duplicate 60 mm plates [Wigler et al., Cell, 14, 725-731 (1978)]. The plasmid V19.8 SCF is shown in Figure 17. As a control, the vector without insert was also transfected. Tissue culture supernatants were harvested
30 at various time points post-transfection and assayed for biological activity. Table 4 summarizes the HPP-CFC bioassay results and Table 5 summarizes the MC/9 ³H-thymidine uptake data from typical transfection experiments. Bioassay results of supernatants from
35 COS-1 cells transfected with the following plasmids are shown in Tables 4 and 5: a C-terminally-truncated form of rat SCF with the C-terminus at amino acid position

162 (V19.8 rat SCF¹⁻¹⁶²), SCF¹⁻¹⁶² containing a glutamic acid at position 81 [V19.8 rat SCF¹⁻¹⁶² (Glu81)], and SCF¹⁻¹⁶² containing an alanine at position 19 [V19.8 rat SCF¹⁻¹⁶² (Ala19)]. The amino acid substitutions were the product of PCR reactions performed in the amplification of rat SCF¹⁻¹⁶² as indicated in Example 3. Individual clones of V19.8 rat SCF¹⁻¹⁶² were sequenced and two clones were found to have amino acid substitutions. As can be seen in Tables 4 and 5, the recombinant rat SCF (also referred to throughout this application as rrat SCF or rrSCF), is active in the bioassays used to purify natural mammalian SCF in Example 1.

Table 4

HPP-CFC Assay of COS-1 Supernatants
from Cells Transfected with Rat SCF DNA

	<u>Sample</u>	<u>Volume of</u> <u>CM Assayed (μl)</u>	<u>Colony</u> <u>#/200,000 cells</u>
20	V19.8 (no insert)	100	0
		50	0
		25	0
		12	0
25	V19.8 rat SCF ¹⁻¹⁶²	100	>50
		50	>50
		25	>50
		12	>50
		6	30
		3	8
30	V19.8 rat SCF ¹⁻¹⁶² (Glu81)	100	26
		50	10
		25	2
		12	0
	V19.8 rat SCF ¹⁻¹⁶² (Ala19)	100	41
		50	18
		25	5
35		12	0
		6	0
		3	0

Table 5
MC/9³H-Thymidine Uptake Assay of COS-1
Supernatants from Cells Transfected with Rat SCF DNA

Sample	Volume of CM Assayed (μl)	cpm
5	v19.8(no insert) 25	1,936
	12	2,252
	6	2,182
	3	1,682
10	v19.8 SCF ¹⁻¹⁶² 25	11,648
	12	11,322
	6	11,482
	3	9,638
15	v19.8 SCF ¹⁻¹⁶² (Glu81) 25	6,220
	12	5,384
	6	3,692
	3	1,980
20	v19.8 SCF ¹⁻¹⁶² (Ala19) 25	8,396
	12	6,646
	6	4,566
	3	3,182

Recombinant rat SCF, and other factors, were tested individually in a human CFU-GM [Broxmeyer et al., supra (1977)] assay which measures the proliferation of normal bone marrow cells and the data are shown in Table 6. Results for COS-1 supernatants from cultures 4 days after transfection with V19.8 SCF¹⁻¹⁶² in combination with other factors are also shown in Table 6. Colony numbers are the average of triplicate cultures.

The recombinant rat SCF has primarily a synergistic activity on normal human bone marrow in the CFU-GM assay. In the experiment in Table 6, SCF synergized with human GM-CSF, human IL-3, and human CSF-1. In other assays, synergy was observed with G-CSF also. There was some proliferation of human bone marrow after 14 days with rat SCF; however, the clusters were composed of <40 cells. Similar results were obtained with natural mammalian-derived SCF.

Table 6
Human CFU-GM Assay of COS-1 Supernatants
from Cells Transfected with Rat SCF DNA

5	Sample	Colony #/100,000 cells (\pm SEM)
	Saline	0
	GM-CSF	7 \pm 1
	G-CSF	24 \pm 1
	IL-3	5 \pm 1
10	CSF-1	0
	SCF ¹⁻¹⁶²	0
	GM-CSF + SCF ¹⁻¹⁶²	29 \pm 6
	G-CSF + SCF ¹⁻¹⁶²	20 \pm 1
	IL-3 + SCF ¹⁻¹⁶²	11 \pm 1
15	CSF-1 + SCF ¹⁻¹⁶²	4 \pm 0

EXAMPLE 5

Expression of Recombinant SCF in Chinese Hamster Ovary Cells

This example relates to a stable mammalian expression system for secretion of SCF from CHO cells (ATCC CCL 61 selected for DHFR-).

A. Recombinant Rat SCF

The expression vector used for SCF production was V19.8 (Figure 17). The selectable marker used to establish stable transformants was the gene for dihydrofolate reductase in the plasmid pDSVE.1. Plasmid pDSVE.1 (Figure 18) is a derivative of pDSVE constructed by digestion of pDSVE by the restriction enzyme SalI and ligation to an oligonucleotide fragment consisting of the two oligonucleotides

5'TCGAC CCGGA TCCCC 3'

3' G GGCCT AGGGG AGCT 5'.

Vector pDSVE is described in commonly owned U.S. Ser. Nos. 025,344 and 152,045 hereby incorporated by reference. The vector portion of V19.8 and pDSVE.1 contain long stretches of homology including a bacterial ColE1 origin of replication and ampicillin resistance gene and the SV40 origin of replication. This overlap may contribute to homologous recombination during the transformation process, thereby facilitating co-transformation.

Calcium phosphate co-precipitates of V19.8 SCF constructs and pDSVE.1 were made in the presence or absence of 10 µg of carrier mouse DNA using 1.0 or 0.1 µg of pDSVE.1 which had been linearized with the restriction endonuclease PvuI and 10 µg of V19.8 SCF as described [Wigler et al., supra (1978)]. Colonies were selected based upon expression of the DHFR gene from pDSVE.1. Colonies capable of growth in the absence of added hypoxanthine and thymidine were picked using cloning cylinders and expanded as independent cell lines. Cell supernatants from individual cell lines were tested in an MC/9 ³H-thymidine uptake assay. Results from a typical experiment are presented in Table 7.

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Table 7
MC/9 ³H-Thymidine Uptake Assay of Stable CHO Cell
Supernatants From Cells Transfected With Rat SCF DNA

Volume of Conditioned		
Transfected DNA	Medium Assayed	cpm
5 V19.8 SCF ¹⁻¹⁶²	25	33,926
	12	34,973
	6	30,657
	3	14,714
	1.5	7,160
10 None	25	694
	12	1,082
	6	880
	3	672
	1	1,354
15		

B. Recombinant Human SCF

20 Expression of SCF in CHO cells was also achieved using
the expression vector pDSVR_α2 which is described in
commonly owned Ser. No. 501,904 filed March 29, 1990,
hereby incorporated by reference. This vector includes
a gene for the selection and amplification of clones
25 based on expression of the DHFR gene. The clone pDSR_α2
SCF was generated by a two step process. The V19.8 SCF
was digested with the restriction enzyme BamHI and the
SCF insert was ligated into the BamHI site of pGEM3.
DNA from pGEM3 SCF was digested with HindIII and SalI
30 and ligated into pDSR_α2 digested with HindIII and
SalI. The same process was repeated for human genes
encoding a COOH-terminus at the amino acid positions
162, 164 and 183 of the sequence shown in Figure 15C.

Genes encoding proteins with the COOH-terminus
35 at position 248 of the sequences shown in Figure 42 and
amino acids 1-220 of the sequence in Figure 44 were

generated as follows: DNA encoding the 1-164 amino acid SCF insert in pGEM3 was isolated by digestion with HindIII and ligated into the HindIII site of M13mp18. The sequence preceding the ATG initiation codon was
5 changed by site directed mutagenesis using the oligonucleotide

5'-TCTTCTTCATGGCGGCGCAAGCTT-3'

and a kit from Amersham (Arlington Heights, IL). The resulting clone was digested with HindIII and the SCF
10 sequences were ligated to pDSRa2 digested with HindIII. This clone was designated pDSRa2-Δ12. The 3' end of this gene was exchanged with the 3' end of the 248 or 220 sequences by digesting pDSRa2-Δ12 with XbaI, =
filling in the resulting ends with DNA polymerase I
15 (Klenow fragment) and dATP, dCTP, dGTP and TTP to generate a blunt end and subsequent digestion with SpeI. The 220 and 248 sequences were digested with DraI, which leaves a blunt end and SpeI. The vector and inserts were then ligated together to generate
20 pDSRa2-Δ23 (248 amino acid sequence) or pDSRa2-Δ220 (220 amino acid sequence). These plasmids were used to generate cell lines by calcium phosphate precipitation as described in Example 5A except that pDSVE.1 was not used for selection.

25 Established cell lines were challenged with methotrexate [Shimke, in Methods in Enzymology, 151 85-104 (1987)] at 10 nM to increase expression levels of the DHFR gene and the adjacent SCF gene. Expression levels of recombinant human SCF were assayed by
30 radioimmune assay, as in Example 7, and/or induction of colony formation in vitro using human peripheral blood leucocytes. This assay is performed as described in Example 9 (Table 12) except that peripheral blood is used instead of bone marrow and the incubation is
35 performed at 20% O₂, 5% CO₂, and 75% N₂ in the presence of human EPO (10 U/ml). Results from typical

experiments are shown in Table 8. The SCF²²⁰ and SCF²⁴⁸ also showed similar expression in these assays and as determined by Western blot analysis. The CHO clone expressing human SCF¹⁻¹⁶⁴ has been deposited on September 25, 1990 with ATCC (CRL 10557) and designated Hu164SCF17.

Table 8

<u>hPBL Colony Assay of Conditioned Media From Stable CHO Cell Lines Transfected With Human SCF DNA</u>		
15	<u>Transfected DNA</u>	<u>Media assayed(μl)</u> <u>Number of Colonies/10⁵</u>
	pDSRα2 hSCF ¹⁻¹⁶⁴	50 53 25 45 12.5 27 6.25 13
20	pDSRα2 hSCF ¹⁻¹⁶²	10 43 5 44 2.5 31 1.25 17 0.625 21
25	None (CHO control)	50 4

30 C. Secreted Product of CHO Cells Transfected with pDSRα2-Δ23.

CHO cells transfected with pDSRα2-Δ23 (248 amino acid sequence; see Example 5B) were cultured as described in Example 11A. As previously described, 35 the sequences shown in Figure 42 include a putative hydrophobic transmembrane region represented by amino

acids numbered 190-212, which could anchor a synthesized protein in the cell membrane. This is also the case for the encoded rat sequences of Figure 14, yet soluble rat SCF representing amino acids 1-164/165 was recovered from conditioned medium of BRL-3A cells as described in Examples 1 and 2. This is indicative of proteolytic processing leading to release of soluble SCF. To study such processing for a case involving the human protein, the CHO cells transfected with pDSRa2-Δ23 were cultured as described in Example 5B. Conditioned medium contained soluble human SCF, which was purified essentially by the methods outlined in Example 11B. By SDS-PAGE, combined with the use of glycosidases as outlined in Examples 10 and 11C, it was found that the behavior of the purified material was much like that described for BRL-3A derived rat SCF (Example 1D) and for human SCF purified from conditioned medium of CHO cells transfected with pDSRa2 human SCF¹⁻¹⁶² (see Example 11C). The mobility on SDS-PAGE of the major band remaining after treatment with neuraminidase, O-glycanase, and N-glycanase was slightly less than the mobility seen for the major band after such treatment of the CHO cell-derived human SCF 1-162 described in Example 11C. This mobility difference corresponded to less than 1000 in molecular weight difference and indicated that the less mobile product was larger by a few amino acids.

The purified material from the CHO cells transfected with pDSRa2-Δ23 was subjected to detailed structural analysis, by methods including those given in Example 2. The N-terminal amino acid sequence is Glu-Gly-Ile..., indicating that it is the product of processing/cleavage between residues indicated as numbers (-1) Thr and (+1) (Glu) in Figure 42.

To determine the precise C-terminal processing site(s), the purified material was subjected to AspN peptidase digestion (20-50 μg SCF in 100-200 μl 0.1 M

sodium phosphate, pH 7.2, for 18 h at 37°C with AspN:SCF ratio of 1:200 by weight) followed by HPLC to isolate resulting peptides. The elution profile shown in Figure 16C was obtained. Collected peptide fractions
5 were sequenced to identify the C-terminal peptide. A peptide eluting at 36.8 min represents the C-terminal peptide. The sequence Asp-Ser-Arg-Val-Ser-Val-(X)-Lys-Pro-Phe-Phe-Met-Leu-Pro-Pro-Val-Ala-(Ala) was assigned, where (X) denotes an unassigned residue, and (Ala)
10 denotes tentative assignment due to low recovery. The indicated amino acids corresponds to position 148-165 of the sequence shown in Figure 42.

After treatment of the C-terminal peptide with α -neuraminidase and O-glycanase to remove carbohydrate,
15 fast atom bombardment - mass spectroscopy (FAB-MS) analysis indicated a molecular weight of 1815.19 for the protonated monoisotopic ion (NH^+), consistent with the sequence Asp-Ser-Arg-Val-Ser-Val-Thr-Lys-Pro-Phe-Phe-Met-Leu-Pro-Pro-Val-Ala-Ala (calculated molecular weight
20 of $\text{MH}^+ = 1815.98$). A less abundant ion species of mass 1744.37, corresponding to the above-mentioned peptide truncated by one Ala at the C-terminus (calculated $\text{MH}^+ = 1744.17$), was also detected.

Further analyses were performed using
25 electrospray mass spectroscopy (ES-MS). The deglycosylated C-terminal peptide fraction of the CHO cell-derived SCF and the C-terminal peptide fraction from E. coli-derived SCF¹⁻¹⁶⁵ (obtained as described in Example 2) were analyzed. A major signal with mass 1815
30 and a second signal with mass 1743 were detected for the peptide of CHO cell-derived SCF. Only an 1814 signal was detected for the peptide of E. coli-derived SCF.

These data indicate that soluble SCF is released from CHO cells transfected with pDSR α 2- Δ 23 by
35 proteolytic cleavage after amino acid 164 or 165. This processing matches that found for BRL-3A cell derived rat SCF (Example 2).

EXAMPLE 6

Expression of Recombinant SCF in E. coli

A. Recombinant Rat SCF

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This example relates to expression in E. coli of SCF polypeptides by means of a DNA sequence encoding [Met⁻¹] rat SCF¹⁻¹⁹³ (Figure 14C). Although any suitable vector may be employed for protein expression using this DNA, the plasmid chosen was pCFM1156 (Figure 19). This plasmid can be readily constructed from pCFM 836 (see U.S. Patent No. 4,710,473 hereby incorporated by reference) by destroying the two endogenous NdeI restriction sites by end-filling with T4 polymerase enzyme followed by blunt end ligation and substituting the small DNA sequence between the unique ClaI and KpnI restriction sites with the small oligonucleotide shown below.

20 5' CGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTAC 3'
3' TAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGC 5'

Control of protein expression in the pCFM1156 plasmid is by means of a synthetic lambda P_L promoter which is itself under the control of a temperature sensitive lambda CI857 repressor gene [such as is provided in E. coli strains FM5 (ATCC deposit #53911) or K12ΔHtrp]. The pCFM1156 vector is constructed so as to have a DNA sequence containing an optimized ribosome binding site and initiation codon immediately 3' of the synthetic PL promoter. A unique NdeI restriction site, which contains the ATG initiation codon, precedes a multi-restriction site cloning cluster followed by a lambda t-cox transcription stop sequence.

35 Plasmid V19.8 SCF¹⁻¹⁹³ containing the rat SCF¹⁻¹⁹³ gene cloned from PCR amplified cDNA

(Figure 14C) as described in Example 3 was digested with BglII and SstII and a 603 bp DNA fragment isolated. In order to provide a Met initiation codon and restore the codons for the first three amino acid residues (Gln, Glu, and Ile) of the rat SCF polypeptide, a synthetic oligonucleotide linker

5' TATGCAGGA 3'
3' ACGTCCTCTAG 5'

with NdeI and BglII sticky ends was made. The small oligonucleotide and rat SCF¹⁻¹⁹³ gene fragment were inserted by ligation into pCFM1156 at the unique NdeI and SstII sites in the plasmid shown in Figure 19. The product of this reaction is an expression plasmid, pCFM1156 rat SCF¹⁻¹⁹³.

The pCFM1156 rat SCF¹⁻¹⁹³ plasmid was transformed into competent FM5 E. coli host cells. Selection for plasmid-containing cells was on the basis of the antibiotic (kanamycin) resistance marker gene carried on the pCFM1156 vector. Plasmid DNA was isolated from cultured cells and the DNA sequence of the synthetic oligonucleotide and its junction to the rat SCF gene confirmed by DNA sequencing.

To construct the plasmid pCFM1156 rat SCF¹⁻¹⁶² encoding the [Met⁻¹] rat SCF¹⁻¹⁶² polypeptide, an EcoRI to SstII restriction fragment was isolated from V19.8 rat SCF¹⁻¹⁶² and inserted by ligation into the plasmid pCFM rat SCF¹⁻¹⁹³ at the unique EcoRI and SstII restriction sites thereby replacing the coding region for the carboxyl terminus of the rat SCF gene.

To construct the plasmids pCFM1156 rat SCF¹⁻¹⁶⁴ and pCFM1156 rat SCF¹⁻¹⁶⁵ encoding the [Met⁻¹] rat SCF¹⁻¹⁶⁴ and [Met⁻¹] rat SCF¹⁻¹⁶⁵ polypeptides, respectively, EcoRI to SstII restriction fragments were isolated from PCR amplified DNA encoding the 3' end of the SCF gene and designed to introduce site directed changes in the DNA in the region encoding the carboxyl

terminus of the SCF gene. The DNA amplifications were performed using the oligonucleotide primers 227-29 and 237-19 in the construction of pCFM1156 rat SCF¹⁻¹⁶⁴ and 227-29 and 237-20 in the construction of pCFM1156 rat SCF¹⁻¹⁶⁵.

B. Recombinant Human SCF

This example relates to the expression in *E. coli* of human SCF polypeptide by means of a DNA sequence encoding [Met⁻¹] human SCF¹⁻¹⁶⁴ and [Met⁻¹] human SCF¹⁻¹⁸³ (Figure 15C); and [Met⁻¹] human SCF¹⁻¹⁶⁵ (Figure 15C). Plasmid V19.8 human SCF¹⁻¹⁶² containing the human SCF¹⁻¹⁶² gene was used as template for PCR amplification of the human SCF gene. Oligonucleotide primers 227-29 and 237-19 were used to generate the PCR DNA which was then digested with PstI and SstII restriction endonucleases. In order to provide a Met initiation codon and restore the codons for the first four amino acid residues (Glu, Gly, Ile, Cys) of the human SCF polypeptide, a synthetic oligonucleotide linker

```
5'   TATGGAAGGTATCTGCA   3'
3'   ACCTTCCATAG       5'
```

with NdeI and PstI sticky ends was made. The small oligo linker and the PCR derived human SCF gene fragment were inserted by ligation into the expression plasmid pCFM1156 (as described previously) at the unique NdeI and SstII sites in the plasmid shown in Figure 19.

The pCFM1156 human SCF¹⁻¹⁶⁴ plasmid was transformed into competent FM5 *E. coli* host cells. Selection for plasmid containing cells was on the basis of the antibiotic (kanamycin) resistance marker gene carried on the pCFM1156 vector. Plasmid DNA was isolated from cultured cells and the DNA sequence of the human SCF gene confirmed by DNA sequencing.

To construct the plasmid pCFM1156 human SCF¹⁻¹⁸³ encoding the [Met⁻¹] human SCF¹⁻¹⁸³ (Figure 15C) polypeptide, a EcoRI to HindIII restriction fragment encoding the carboxyl terminus of the human SCF gene was isolated from pGEM human SCF¹¹⁴⁻¹⁸³ (described below), a SstI to EcoRI restriction fragment encoding the amino terminus of the human SCF gene was isolated from pCFM1156 human SCF¹⁻¹⁶⁴, and the larger HindIII to SstI restriction fragment from pCFM1156 was isolated.

10 The three DNA fragments were ligated together to form the pCFM1156 human SCF¹⁻¹⁸³ plasmid which was then transformed into FM5 E. coli host cells. After colony selection using kanamycin drug resistance, the plasmid DNA was isolated and the correct DNA sequence confirmed

15 by DNA sequencing. The pGEM human SCF¹¹⁴⁻¹⁸³ plasmid is a derivative of pGEM3 that contains an EcoRI-SphI fragment that includes nucleotides 609 to 820 of the human SCF cDNA sequence shown in Figure 15C. The EcoRI-SphI insert in this plasmid was isolated from a

20 PCR that used oligonucleotide primers 235-31 and 241-6 (figure 12B) and PCR 22.7 (Figure 13B) as template. The sequence of primer 241-6 was based on the human genomic sequence to the 3' side of the exon containing the codon for amino acid 176.

25 A plasmid encoding human [Met⁻¹] SCF¹⁻¹⁶⁵ was constructed as follows. Sixteen oligonucleotides were "stitched together" to create a 221 base pair fragment with EcoRI and BamHI sticky ends (Figure 16D). This nucleotide sequence codes for the C-terminal 68 amino

30 acids of human SCF¹⁻¹⁸³ (amino acid numbering and designation as in Figure 15C). The codons in this nucleotide sequence reflected those most commonly used by E. coli (i.e., optimized for expression in E. coli). In addition, a unique BstEII site is present

35 in the fragment. The EcoRI to BamHI fragment of the human SCF¹⁻¹⁸³ DNA (Figure 15C) was removed and replaced

by the fragment containing the optimized codons. This construct was digested with BstEII and BamHI and the 39 base pair fragment shown in Figure 16E was introduced. The resulting plasmid codes for human [Met⁻¹] SCF¹⁻¹⁶⁵ with the codons for the C-terminal 50 amino acids optimized for expression in E. coli.

Another plasmid encoding human [Met⁻¹] SCF¹⁻¹⁶⁵, with the codons of Figure 15C, was also constructed, by PCR utilizing pCFM1156 human SCF¹⁻¹⁶⁴. A 5' oligonucleotide was made 5' of the EcoRI site and a 3' oligonucleotide was made which included the final codons of the 1-164 sequence plus an extra codon for the position 165 and nucleotides through the SstII site. After the PCR reaction, the fragment was cut with EcoRI and SstII, gel purified, and cloned into pCFM1156 human SCF¹⁻¹⁶⁴ cut with EcoRI and SstII.

The generation of other expression plasmids including those encoding human [Met⁻¹] SCF¹⁻²⁴⁸ (sequence of Figure 42) and encoding human [Met⁻¹] SCF¹⁻²²⁰ (sequence of Figure 44) is described in Example 28.

C. Fermentation of E. coli producing Human SCF¹⁻¹⁶⁴ and E. coli producing Human SCF¹⁻¹⁶⁵

Fermentations for the production of SCF¹⁻¹⁶⁴ were carried out in 16 liter fermentors using an FM5 E. coli K12 host containing the plasmid pCFM 1156 human SCF¹⁻¹⁶⁴. Seed stocks of the producing culture were maintained at -80° C in 17% glycerol in Luria broth. For inoculum production, 100 µl of the thawed seed stock was transferred to 500 ml of Luria broth in a 2 L erlenmeyer flask and grown overnight at 30°C on a rotary shaker (250 RPM).

For the production of E. coli cell paste used as starting material for the purification of human

SCF¹⁻¹⁶⁴ outlined in Example 10, the following fermentation conditions were used.

The inoculum culture was aseptically transferred to a 16 L fermentor containing 8 L of batch medium (see Table 9). The culture was grown in batch mode until the OD-600 of the culture was approximately 3-5. At this time, a sterile feed (Feed 1, Table 10) was introduced into the fermentor using a peristaltic pump to control the feed rate. The feed rate was increased exponentially with time to give a growth rate of 0.15 hr⁻¹. The temperature was controlled at 30°C during the growth phase. The dissolved oxygen concentration in the fermentor was automatically controlled at 50% saturation using air flow rate, agitation rate, vessel back pressure and oxygen supplementation for control. The pH of the fermentor was automatically controlled at 7.0 using phosphoric acid and ammonium hydroxide. At an OD-600 of approximately 30, the production phase of the fermentation was induced by increasing the fermentor temperature to 42°C. At the same time the addition of Feed 1 was stopped and the addition of Feed 2 (Table 11) was started at a rate of 200 ml/hr. Approximately six hours after the temperature of the fermentor was increased, the fermentor contents were chilled to 15°C. The yield of SCF¹⁻¹⁶⁴ was approximately 30 mg/OD-L. The cell pellet was then harvested by centrifugation in a Beckman J6-B rotor at 3000 x g for one hour. The harvested cell paste was stored frozen at -70°C.

An advantageous method for production of SCF¹⁻¹⁶⁴ is similar to the method described above except for the following modifications.

1) The addition of Feed 1 is not initiated until the OD-600 of the culture reaches 5-6.

2) The rate of addition of Feed 1 is increased more slowly, resulting in a slower growth rate (approximately 0.08).

3) The culture is induced at OD-600 of 20.

5 4) Feed 2 is introduced into the fermentor at a rate of 300 mL/hr.

All other operations are similar to the method described above, including the media.

10 Using this process, yields of SCF¹-164 approximately 35-40 mg/OD-L at OD=25 have been obtained.

TABLE 9

Composition of Batch Medium

15	Yeast extract	10 ^a g/L
	Glucose	5
	K ₂ HPO ₄	3.5
	KH ₂ PO ₄	4
20	MgSO ₄ ·7H ₂ O	1
	NaCl	0.625
	Dow P-2000 antifoam	5 mL/8 L
	Vitamin solution ^b	2 mL/L
	Trace metals solution ^c	2 mL/L

25 ^aUnless otherwise noted, all ingredients are listed as g/L.

^bTrace Metals solution: FeCl₃·6H₂O, 27 g/L; ZnCl₂·4
30 H₂O, 2g/L; CaCl₂·6H₂O, 2 g/L; Na₂MoO₄·2 H₂O, 2 g/L,
CuSO₄·5 H₂O, 1.9 g/L; concentrated HCl, 100 ml/L.

^cVitamin solution: riboflavin, 0.42 g/l; pantothenic
acid, 5.4 g/L; niacin, 6 g/L; pyridoxine, 1.4 g/L;
35 biotin, 0.06 g/L; folic acid, 0.04 g/L.

TABLE 10

Composition of Feed Medium

5	Yeast extract	50 ^a
	Glucose	450
	MgSO ₄ ·7H ₂ O	8.6
	Trace metals solution ^b	10 mL/L
	Vitamin solution ^c	10 mL/L
10	^a Unless otherwise noted, all ingredients are listed as g/L.	
	^b Trace Metals solution: FeCl ₃ ·6H ₂ O, 27 g/L; ZnCl ₂ ·4	
15	H ₂ O, 2g/L; CaCl ₂ ·6H ₂ O, 2 g/L; Na ₂ MoO ₄ ·2 H ₂ O, 2 g/L, CuSO ₄ ·5 H ₂ O, 1.9 g/L; concentrated HCl, 100 ml/L.	
	^c Vitamin solution: riboflavin, 0.42 g/l; pantothenic acid, 5.4 g/L; niacin, 6 g/L; pyridoxine, 1.4 g/L;	
20	biotin, 0.06 g/L; folic acid, 0.04 g/L.	

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TABLE 11

Composition of Feed Medium 2

5	Tryptone	172 ^a
	Yeast extract	86
	Glucose	258

^aAll ingredients are listed as g/L.

10

For the production of E. coli cell paste used as starting material for the purification of human SCF¹-165 (Example 10), fermentation conditions differed in the following ways from those described for the SCF¹-164 cases. Feed 1 was introduced when the OD-600 of the culture was approximately 5-6. Feed 1 contained 13 g/L K₂HPO₄ in addition to the components listed in Table 10. The feed rate was increased exponentially with time to give a growth rate of 0.2 hr⁻¹. Production phase was induced by temperature increase at OD-600 of about 40, and the rate of addition of Feed 2 was 600 ml/hr. Feed 2 contained 258 g/L tryptone, 129 g/L yeast extract, 50 g/L glucose, and 6.4 g/L K₂HPO₄. Chilling of the fermentor and harvesting of cells was done about eight hours after the temperature increase.

EXAMPLE 7

Immunoassays for Detection of SCF

30

Radioimmunoassay (RIA) procedures applied for quantitative detection of SCF in samples were conducted according to the following procedures.

An SCF preparation from BRL 3A cells purified as in Example 1 was incubated together with antiserum for two hours at 37°C. After the two hour incubation, the sample tubes were then cooled on ice, ¹²⁵I-SCF was

35

added, and the tubes were incubated at 4°C for at least 20 h. Each assay tube contained 500 µl of incubation mixture consisting of 50 µl of diluted antisera, -60,000 5 µl trasylol and 0-400 µl of SCF standard, with buffer (phosphate buffered saline, 0.1% bovine serum albumin, 0.05% Triton X-100, 0.025% azide) making up the remaining volume. The antiserum was the second test bleed of a rabbit immunized with a 50% pure preparation of natural SCF from BRL 3A conditioned medium. The 10 final antiserum dilution in the assay was 1:2000.

The antibody-bound ^{125}I -SCF was precipitated by the addition of 150 µl Staph A (Calbiochem). After a 1 h incubation at room temperature, the samples were centrifuged and the pellets were washed twice with 15 0.75 ml 10 mM Tris-HCL pH 8.2, containing 0.15M NaCl, 2 mM EDTA, and 0.05% Triton X-100. The washed pellets were counted in a gamma counter to determine the percent of ^{125}I -SCF bound. Counts bound by tubes lacking serum were subtracted from all final values to correct for 20 nonspecific precipitation. A typical RIA is shown in Figure 20. The percent inhibition of ^{125}I -SCF binding produced by the unlabeled standard is dose dependent (Figure 20A), and, as indicated in Figure 20B, when the immune precipitated pellets are examined by SDS-PAGE and 25 autoradiography, the ^{125}I -SCF protein band is competed. In Figure 20B, lane 1 is ^{125}I -SCF, and lanes 2, 3, 4 and 5 are immune-precipitated ^{125}I -SCF competed with 0, 2, 100, and 200 ng of SCF standard, respectively. As determined by both the decrease in 30 antibody-precipitable cpm observed in the RIA tubes and decrease in the immune-precipitated ^{125}I -SCF protein band (migrating at approximately M_r 31,000) the polyclonal antisera recognizes the SCF standard which was purified as in Example 1.

35 Western procedures were also applied to detect recombinant SCF expressed in E. coli, COS-1, and CHO

cells. Partially purified E. coli expressed rat SCF¹⁻¹⁹³ (Example 10), COS-1 cell expressed rat SCF¹⁻¹⁶² and SCF¹⁻¹⁹³ as well as human SCF¹⁻¹⁶² (Examples 4 and 9), and CHO cell expressed rat SCF¹⁻¹⁶² (Example 5), were subjected to SDS-PAGE. Following electrophoresis, the protein bands were transferred to 0.2 μ m nitrocellulose using a Bio-Rad Transblot apparatus at 60V for 5 h. The nitrocellulose filters were blocked for 4 h in PBS, pH 7.6, containing 10% goat serum followed by a 14 h room temperature incubation with a 1:200 dilution of either rabbit preimmune or immune serum (immunization described above). The antibody-antiserum complexes were visualized using horseradish peroxidase-conjugated goat anti-rabbit IgG reagents (Vector laboratories) and 4-chloro-1-naphthol color development reagent.

Examples of two Western analyses are presented in Figures 21 and 22. In Figure 21, lanes 3 and 5 are 200 μ l of COS-1 cell produced human SCF¹⁻¹⁶²; lanes 1 and 7 are 200 μ l of COS-1 cell produced human EPO (COS-1 cells transfected with V19.8 EPO); and lane 8 is prestained molecular weight markers. Lanes 1-4 were incubated with pre-immune serum and lanes 5-8 were incubated with immune serum. The immune serum specifically recognizes a diffuse band with an apparent M_r of 30,000 daltons from COS-1 cells producing human SCF¹⁻¹⁶² but not from COS-1 cells producing human EPO.

In the Western shown in Figure 22, lanes 1 and 7 are 1 μ g of a partially purified preparation of rat SCF¹⁻¹⁹³ produced in E. coli; lanes 2 and 8 are wheat germ agglutinin-agarose purified COS-1 cell produced rat SCF¹⁻¹⁹³; lanes 4 and 9 are wheat germ agglutinin-agarose purified COS-1 cell produced rat SCF¹⁻¹⁶²; lanes 5 and 10 are wheat germ agglutinin-agarose purified CHO cell produced rat SCF¹⁻¹⁶²; and lane 6 is prestained molecular weight markers. Lanes 1-5 and lanes 6-10 were

incubated with rabbit preimmune and immune serum,
respectively. The E. coli produced rat SCF¹⁻¹⁹³ (lanes
1 and 7) migrates with an apparent M_r of ~24,000 daltons
while the COS-1 cell produced rat SCF¹⁻¹⁹³ (lanes 2 and
5 8) migrates with an apparent M_r of 24-36,000 daltons.
This difference in molecular weights is expected since
mammalian cells, but not bacteria, are capable of
glycosylation. Transfection of the sequence encoding
rat SCF¹⁻¹⁶² into COS-1 (lanes 4 and 9), or CHO cells
10 (lanes 5 and 10), results in expression of SCF with a
lower average molecular weight than that produced by
transfection with SCF¹⁻¹⁹³ (lanes 2 and 8).

The expression products of rat SCF¹⁻¹⁶² from
COS-1 and CHO cells are a series of bands ranging in
15 apparent M_r between 24-36,000 daltons. The
heterogeneity of the expressed SCF is likely due to
carbohydrate variants, where the SCF polypeptide is
glycosylated to different extents.

In summary, Western analyses indicate that
20 immune serum from rabbits immunized with natural
mammalian SCF recognize recombinant SCF produced in
E. coli, COS-1 and CHO cells but fail to recognize any
bands in a control sample consisting of COS-1 cell
produced EPO. In further support of the specificity of
25 the SCF antiserum, preimmune serum from the same rabbit
failed to react with any of the rat or human SCF
expression products.

Radioimmunoassay (RIA) procedures were also
developed to quantify SCF in human serum samples.
30 Purified CHO-derived human SCF (expression of the 1-248
transcript) was used as the standard in this assay over
the range of 0.01-10.0 ng/tube. Pooled normal human
serum samples, obtained from Irvine Scientific (Lots
500080713 and 500081015), were each assayed at 25, 50,
35 100 and 200 μ l per tube. Each tube was adjusted to
contain 5 μ l of trasylol, and 900 μ l total volume by the

addition of the appropriate amount of assay diluent (phosphate-buffered saline containing 0.1% bovine serum albumin and 0.025% sodium azide). Rabbit anti-human SCF antiserum (100 μ l of a 1:50,000 dilution) was added, the
5 tubes were mixed and incubated at 4°C for approximately 24 hours. The antiserum was the bleed-out of a rabbit hyperimmunized with a purified preparation of CHO-derived human SCF¹⁻¹⁶².

Following the 24 hours incubation,
10 approximately 60,000 cpm of ¹²⁵I-CHO-derived human SCF (expression of the 1-248 transcript, 57.9 mCi/mg) was added to all tubes; the tubes were vortexed and incubated at 4°C for an additional 19 hours. The
15 antibody-bound ¹²⁵I-human SCF was precipitated by the addition of 100 μ l of a 1:50 dilution of normal rabbit serum (Research Products International) and 100 μ l of a 1:20 dilution of goat anti-rabbit IgG (Research Products International) to all tubes. After a two hour
20 incubation at room temperature, the tubes were centrifuged and the pellets were washed once with 0.75 ml of 10 mM Tris-HCl, pH 8.2, containing 0.15 M NaCl, 2 mM EDTA, and 0.05% Triton X-100. The washed pellets
25 were counted in a gamma counter to determine the percent of ¹²⁵I-human SCF bound. Counts bound by tubes lacking antiserum were subtracted from all final values to
correct for nonspecific precipitation. A typical RIA is shown in Figure 22A. The percent inhibition of ¹²⁵I-human SCF binding by the unlabeled standard and normal
30 human serum was dose-dependent. Increasing aliquots of the normal human serum, over the range of 25-200 μ l produced a dose response line which was parallel to that of the standard. Both of the normal human serum samples
were assayed twice in this assay. Values plotted in
35 Figure 22A are the average percent inhibitions obtained for the respective aliquots for each serum sample. Values of 2.16 ng/ml and 2.93 ng/ml were obtained for

SCF levels in Lot 500080713 and Lot 500081015 normal human serum, respectively.

EXAMPLE 8

5

In Vivo Activity of Recombinant SCF

A. Rat SCF in Bone Marrow Transplantation

COS-1 cells were transfected with V19.8
10 SCF¹⁻¹⁶² in a large scale experiment (T175 cm² flasks instead of 60 mm dishes) as described in Example 4. Approximately 270 ml of supernatant was harvested. This supernatant was chromatographed on wheat germ
agglutinin-agarose and S-Sepharose essentially as
15 described in Example 1. The recombinant SCF was evaluated in a bone marrow transplantation model based on murine W/W^V genetics. The W/W^V mouse has a stem cell defect which among other features results in a macrocytic anemia (large red cells) and allows for the
20 transplantation of bone marrow from normal animals without the need for irradiation of the recipient animals [Russel, et al., Science, 144, 844-846 (1964)]. The normal donor stem cells outgrow the defective recipient cells after transplantation.

25 In the following example, each group contained six age matched mice. Bone marrow was harvested from normal donor mice and transplanted into W/W^V mice. The blood profile of the recipient animals is followed at different times post transplantation and engraftment of
30 the donor marrow is determined by the shift of the peripheral blood cells from recipient to donor phenotype. The conversion from recipient to donor phenotype is detected by monitoring the forward scatter profile (FASCAN, Becton Dickinson) of the red blood
35 cells. The profile for each transplanted animal was compared to that for both donor and recipient un-

transplanted control animals at each time point. The comparison was made utilizing a computer program based on Kolmogorov-Smirnov statistics for the analysis of histograms from flow systems [Young, J. Histochem. and Cytochem., 25, 935-941 (1977)]. An independent
5 qualitative indicator of engraftment is the hemoglobin type detected by hemoglobin electrophoresis of the recipient blood [Wong, et al., Mol. and Cell. Biol., 9, 798-808 (1989)] and agrees well with the goodness of fit
10 determination from Kolmogorov-Smirnov statistics.

Approximately 3×10^5 cells were transplanted without SCF treatment (control group in Figure 23) from C56BL/6J donors into W/W^V recipients. A second group
received 3×10^5 donor cells which had been treated with
15 SCF (600 U/ml) at 37°C for 20 min and injected together (pre-treated group in Figure 23). (One unit of SCF is defined as the amount which results in half-maximal stimulation in the MC/9 bioassay). In a third group, the recipient mice were injected sub-cutaneously (sub-Q)
20 with approximately 400 U SCF/day for 3 days after transplantation of 3×10^5 donor cells (Sub-Q inject group in Figure 23). As indicated in Figure 23, in both SCF-treated groups the donor marrow is engrafted faster than in the untreated control group. By 29 days post-
25 transplantation, the SCF pre-treated group had converted to donor phenotype. This Example illustrates the usefulness of SCF therapy in bone marrow transplantation.

B. In vivo activity of Rat SCF in Steel Mice

30

Mutations at the *S1* locus cause deficiencies in hematopoietic cells, pigment cells, and germ cells. The hematopoietic defect is manifest as reduced numbers of red blood cells [Russell, In: Al Gordon,
35 Regulation of Hematopoiesis, Vol. I, 649-675 Appleton-Century-Crafts, New York (1970)], neutrophils

[Ruscetti, Proc. Soc. Exp. Biol. Med., 152, 398 (1976)], monocytes [Shibata, J. Immunol. 135, 3905 (1985)], megakaryocytes [Ebbe, Exp. Hematol., 6, 201 (1978)], natural killer cells [(Clark, Immunogenetics, 12, 601 (1981)], and mast cells [Hayashi, Dev. Biol., 109, 234 (1985)]. Steel mice are poor recipients of a bone marrow transplant due to a reduced ability to support stem cells [Bannerman, Prog. Hematol., 8, 131 (1973)]. The gene encoding SCF is deleted in Steel (Sl/Sl) mice.

Steel mice provide a sensitive in vivo model for SCF activity. Different recombinant SCF proteins were tested in Steel-Dickie (Sl/Sl^d) mice for varying lengths of time. Six to ten week old Steel mice (WCB6F1-Sl/Sl^d) were purchased from Jackson Labs, Bar Harbor, ME. Peripheral blood was monitored by a SYSMEX F-800 microcell counter (Baxter, Irvine, CA) for red cells, hemoglobin, and platelets. For enumeration of peripheral white blood cell (WBC) numbers, a Coulter Channelyzer 256 (Coulter Electronics, Marietta, GA) was used.

In the experiment in Figure 24, Steel-Dickie mice were treated with E. coli derived SCF¹⁻¹⁶⁴, purified as in Example 10, at a dose of 100 µg/kg/day for 30 days, then at a dose of 30 µg/kg/day for an additional 20 days. The protein was formulated in injectable saline (Abbott Labs, North Chicago, IL) +0.1% fetal bovine serum. The injections were performed daily, subcutaneously. The peripheral blood was monitored via tail bleeds of ~50 µl at the indicated times in Figure 24. The blood was collected into 3% EDTA coated syringes and dispensed into powdered EDTA microfuge tubes (Brinkmann, Westbury, NY). There is a significant correction of the macrocytic anemia in the treated animals relative to the control animals. Upon cessation of treatment, the treated animals return to the initial state of macrocytic anemia.

In the experiment shown in Figure 25 and 26, Steel-Dickie mice were treated with different recombinant forms of SCF as described above, but at a dose of 100 µg/kg/day for 20 days. Two forms of E. coli derived rat SCF, SCF¹⁻¹⁶⁴ and SCF¹⁻¹⁹³, were produced as described in Example 10. In addition, E. coli SCF¹⁻¹⁶⁴, modified by the addition of polyethylene glycol (SCF¹⁻¹⁶⁴ PEG25) as in Example 12, was also tested. CHO derived SCF¹⁻¹⁶² produced as in Example 5 and purified as in Example 11, was also tested. The animals were bled by cardiac puncture with 3% EDTA coated syringes and dispensed into EDTA powdered tubes. The peripheral blood profiles after 20 days of treatment are shown in Figure 25 for white blood cells (WBC) and Figure 26 for platelets. The WBC differentials for the SCF¹⁻¹⁶⁴ PEG25 group are shown in Figure 27. There are absolute increases in neutrophils, monocytes, lymphocytes, and platelets. The most dramatic effect is seen with SCF¹⁻¹⁶⁴ PEG 25.

An independent measurement of lymphocyte subsets was also performed and the data is shown in Figure 28. The murine equivalent of human CD4, or marker of T helper cells, is L3T4 [Dialynas, J. Immunol., 131, 2445 (1983)]. LyT-2 is a murine antigen on cytotoxic T cells [Ledbetter, J. Exp. Med., 153, 1503 (1981)]. Monoclonal antibodies against these antigens were used to evaluate T cell subsets in the treated animals.

Whole blood was stained for T lymphocyte subsets as follows. Two hundred microliters of whole blood was drawn from individual animals into EDTA treated tubes. Each sample of blood was lysed with sterile deionized water for 60 seconds and then made isotonic with 10X Dulbecco's Phosphate Buffered Saline (PBS) (Gibco, Grand Island, NY). This lysed blood was washed 2 times with 1X PBS (Gibco, Grand Island, NY) supplemented

with 0.1% Fetal Bovine Serum (Flow Laboratory, McLean, VA) and 0.1% sodium azide. Each sample of blood was deposited into round bottom 96 well cluster dishes and centrifuged. The cell pellet (containing $2-10 \times 10^5$ cells) was resuspended with 20 microliters of Rat anti-Mouse L3T4 conjugated with phycoerythrin (PE) (Becton Dickinson, Mountain View, CA) and 20 microliters of Rat anti-Mouse Lyt-2 conjugated with Fluorescein Isothiocyanate incubated on ice (4°C) for 30 minutes (Becton Dickinson). Following incubation the cells were washed 2 times in 1X PBS supplemented as indicated above. Each sample of blood was then analyzed on a FACScan cell analysis system (Becton Dickinson, Mountain View, CA). This system was standardized using standard autocompensation procedures and Calibrite Beads (Becton Dickinson, Mountain View, CA). These data indicated an absolute increase in both helper T cell populations as well as cytotoxic T cell numbers.

20 C. In Vivo Activity of SCF in Primates

Human SCF¹⁻¹⁶⁴ expressed in E. coli (Example 6B) and purified to homogeneity as in Example 10, was tested for in vivo biological activity in normal primates. Adult male baboons (Papio sp.) were studied in three groups: untreated, n=3; SCF 100 ug/kg/day, n=6; and SCF 30 ug/kg/day, n=6. The treated animals received single daily subcutaneous injections of SCF. Blood specimens were obtained from the animals under ketamine restraint. Specimens for complete blood count, reticulocyte count, and platelet count were obtained on days 1, 6, 11, 15, 20 and 25 of treatment.

All animals survived the protocol and had no adverse reactions to SCF therapy. The white blood cell count increased in the 100 ug/kg treated animals as depicted in Figure 29. The differential count, obtained

manually from Wright Giemsa stained peripheral blood smears, is also indicated in Figure 29. There was an absolute increase in neutrophils, lymphocytes, and monocytes. As indicated in Figure 30 there was also an increase at the 100 ug/kg dose in the hemtocrits as well as platelets.

Human SCF (hSCF¹⁻¹⁶⁴ modified by the addition of polyethylene glycol as in Example 12) was also tested in normal baboons, at a dose of 200 ug/kg-day, administered by continuous intravenous infusion and compared to the unmodified protein. The animals started SCF at day 0 and were treated for 28 days. The results for the peripheral WBC are given in the following table. The PEG modified SCF elicited an earlier rise in peripheral WBC than the unmodified SCF. The same results are obtained with human SCF¹⁻¹⁶⁵ modified by the addition of polyethylene glycol.

Treatment with 200 ug/kg-day hSCF¹⁻¹⁶⁴.

	Animal # M88320		Animal # M88129	
	DAY	WBC	DAY	WBC
	0	5800	0	6800
	+7	10700	+7	7400
25	+14	12600	+14	20900
	+16	22000	+21	18400
	+22	31100	+23	24900
	+24	28100	+29	13000
	+29	9600	+30	23000
30	+36	6600	+37	12100
	+43	5600	+44	10700
			+51	7800

Treatment with 200 µg/kg-day PEG-hSCF¹⁻¹⁶⁴:

		<u>Animal # M88350</u>		<u>Animal # M89116</u>	
		DAY	WBC	DAY	WBC
5		-7	12400	-5	7900
		-2	11600	0	7400
		+4	24700	+6	16400
		+7	20400	+9	17100
		+11	24700	+13	18700
10		+14	32600	+16	19400
		+18	33600	+20	27800
		+21	26400	+23	20700
		+25	16600	+27	20200
		+28	26900	+29	18600
15		+32	9200	+33	7600

Human SCF¹⁻¹⁶⁵ expressed in E. coli (Example 6) and purified to homogeneity as in Example 10B, demonstrates the same in vivo biological activity in primates as E. coli derived recombinant human SCF¹⁻¹⁶⁴.

EXAMPLE 9

In vitro Activity of Recombinant Human SCF

25 A. Human bone marrow assay, murine HPP-CFC assay, and murine MC/9 assay.

The cDNA of human SCF corresponding to amino acids 1-162 obtained by PCR reactions outlined in Example 3D, was expressed in COS-1 cells as described for the rat SCF in Example 4. COS-1 supernatants were assayed on human bone marrow as well as in the murine HPP-CFC and MC/9 assays. The human protein was not active at the concentrations tested in either murine assay; however, it was active on human bone marrow. The culture conditions of the assay were as follows: human bone marrow from healthy volunteers was centrifuged over Ficoll-Hypaque gradients

(Pharmacia) and cultured in 2.1% methyl cellulose, 30% fetal calf serum, 6×10^{-5} M 2-mercaptoethanol, 2 mM glutamine, ISCOVE'S medium (GIBCO), 20 U/ml EPO, and 1×10^5 cells/ml for 14 days in a humidified atmosphere containing 7% O₂, 10% CO₂, and 83% N₂. The colony numbers generated with recombinant human and rat SCF COS-1 supernatants are indicated in Table 12. Only those colonies of 0.2 mm in size or larger are indicated.

Table 12

Growth of Human Bone Marrow Colonies
in Response to SCF

	Plasmid Transfected	Volume of CM Assayed (ul)	- Colony #/100,000 cells \pm SD
15	V19.8 (no insert)	100 50	0 0
	V19.8 human SCF ¹⁻¹⁶²	100 50	33 \pm 7 22 \pm 3
	V19.8 rat SCF ¹⁻¹⁶²	100 50	13 \pm 1 10
20			

The colonies which grew over the 14 day period are shown in Figure 31A (magnification 12x). The arrow indicates a typical colony. The colonies resembled the murine HPP-CFC colonies in their large size (average 0.5 mm). Due to the presence of EPO, some of the colonies were hemoglobinized. When the colonies were isolated and centrifuged onto glass slides using a Cytospin (Shandon) followed by staining with Wright-Giemsa, the predominant cell type was an undifferentiated cell with a large nucleus:cytoplasm ratio as shown in Figure 31B (magnification 400x). The arrows in Figure 31B point to the following structures: arrow 1, cytoplasm; arrow 2, nucleus; arrow 3, vacuoles. Immature cells as a class are large and the cells become progressively smaller as they mature [Diggs et al., The

Morphology of Human Blood Cells, Abbott Labs, 3
(1978)]. The nuclei of early cells of the hemotopoietic
maturation sequence are relatively large in relation to
the cytoplasm. In addition, the cytoplasm of immature
5 cells stains darker with Wright-Giemsa than does the
nucleus. As cells mature, the nucleus stains darker than
the cytoplasm. The morphology of the human bone marrow
cells resulting from culture with recombinant human SCF
is consistent with the conclusion that the target and
10 immediate product of SCF action is a relatively immature
hematopoietic progenitor.

Recombinant human SCF was tested in agar
colony assays on human bone marrow in combination with
other growth factors as described above. The results
15 are shown in Table 13. SCF synergizes with G-CSF,
GM-CSF, IL-3, and EPO to increase the proliferation of
bone marrow targets for the individual CSFs.

TABLE 13.

20

Recombinant human SCF Synergy with Other
Human Colony Stimulating Factors

Colony #/10⁵ cells (14 Days)

25

	mock	0
	hG-CSF	32 ± 3
	hG-CSF + hSCF	74 ± 1
	hGM-CSF	14 ± 2
30	hGM-CSF + hSCF	108 ± 5
	hIL-3	23 ± 1
	hIL-3 + hSCF	108 ± 3
	hEPO	10 ± 5
	hEPO + IL-3	17 ± 1
35	hEPO + hSCF	86 ± 10
	hSCF	0

Another activity of recombinant human SCF is the ability to cause proliferation in soft agar of the human acute myelogenous leukemia (AML) cell line, KG-1 (ATCC CCL 246). COS-1 supernatants from transfected
5 cells were tested in a KG-1 agar cloning assay [Koeffler et al., Science, 200, 1153-1154 (1978)] essentially as described except cells were plated at 3000/ml. The data from triplicate cultures are given in Table 14.

10

Table 14

KG-1 Soft Agar Cloning Assay

	Plasmid Transfected	Volume Assayed (ul)	Colony #/3000 Cells \pm SD
15	V19.8 (no insert)	25	2 \pm 1
	V19.8 human SCF ¹⁻¹⁶²	25	14 \pm 0
		12	8 \pm 0
		6	9 \pm 5
		3	6 \pm 4
20		1.5	6 \pm 6
	V19.8 rat SCF ¹⁻¹⁶²	25	6 \pm 1
	human GM-CSF	50 (5 ng/ml)	14 \pm 5

25 B. UT-7 ³H-Thymidine Uptake Assay

UT-7 cells are a human megakaryocyte, huGM-CSF responsive cell line obtained from John Adamson, New York Blood Center, New York, New York. UT-7 cells
30 were cultured in Iscove's Modified Dulbecco's Medium, 10% FBS, 1 x glutamine, 5 \g/ml huGM-CSF. Cells are passaged twice a week at 1 x 10⁵ cells/ml.

Cells were washed twice in phosphate buffered saline (PBS) and resuspended in RPMI medium with 4% FBS
35 and glutamine penicillin streptomycin (GPS) (Irvine Scientific Cat No. 9316 used at 1% volume per volume) at

4 x 10⁴ cells/ml before use. Human SCF along with specific samples were added to 4000 cells/well in 96 well plates and were cultured for 72 hrs. 0.5 uCi/well of ³H-Thymidine was then added to each plate, plates
5 were harvested and counted 4 hours later. A typical assay is shown in Figure 31C.

Activity of human [Met⁻¹]SCF¹⁻¹⁶⁴ and human [Met⁻¹]SCF¹⁻¹⁶⁵, prepared from E. coli as described in Example 10, are also equally active in stimulating
10 the proliferation of the UT-7 cell line, as shown in Figure 31C.

C. SCF Radio-Receptor Assay Protocol

15 OCIM1 cells, [Papayannopoulou et al., Blood 72:1029-1038 (1988)] are a human erythroleukemic cell line expressing many human SCF receptors per cell. These cells are grown in Iscove's Modified Dulbecco's Medium, 10% FBS, and 1x glutamine and passaged 3 times a
20 week to 1 x 10⁵ cells/ml.

Preparation of the OCIM1 plasma membrane is as follows with all steps performed on ice.

First, 40 T175 flasks of cells were grown-up in OCIM1 culture medium, for a total of 1.9 x 10⁹
25 cells/ml. The conditioned medium and 1 mM Phenyl Methyl Sulfonyl Fluoride (PMSF) protease inhibitor, was spun down in 8 x 250 ml tubes at 1000 rpm for 10 minutes at 4°C. Cells were washed with PBS and repelleted in 4 x 50 ml centrifuge tubes at 1000 rpm for 10 minutes at
30 4°C. Cells were resuspended in 20 ml ice cold PBS with glucose sodium pyruvate (Gibco Cat # 310-4287). The 20 ml cell solution was put into a pre-pressurized, pre-chilled (4°C) "cell bomb" designed to lyse the cells. Cells were pressurized at 400-650 PSI for 10 minutes to
35 establish equilibrium. When the pressure is released cell lysis occurs.

At this point the cells were checked for the percentage of cell lysis. 90% lysis was common. The cell suspension was resuspended in 80 mls sucrose buffer (0.25M sucrose, 10 mM Tris, 1mM EDTA in double distilled (dd) H₂O, filtered through a 0.45u filter, pH 7.0) and divided between two 40ml screwcap tubes. Tubes were spun at 5900 RPM for 10 minutes in a Beckman J2-21 centrifuge, JA-20 rotor at 4°C. The supernatants were saved and spun one more time as above to further remove any unwanted material. Supernatants were saved and distributed equally into 2 nalgene 40ml centrifuge tubes. These supernatants were centrifuged at 16,000 RPM 4°C for 30 min. in J2-21 centrifuge, JA-20 rotor. These supernatants were discarded being careful to save pellets. Each pellet was resuspended in sucrose buffer so there were 20mls per tube in 4 x 36ml plastic ultracentrifuge tubes. Using a 20 ml syringe and a large trochar, the solution was carefully underlayered in each tube with ice cold 36% sucrose solution (36.1g sucrose/100mls ddH₂O), bringing the level of the liquid to within 2mm of the top of the tube. Without disturbing the interface, each tube was carefully placed into each of 6 titanium ultracentrifuge tubes. Tubes were centrifuged at 27,000 RPM, 4°C for 75 minutes in an ultracentrifuge. These tubes were carefully removed from the rotor and from titanium buckets, placed in a rack with the 36% sucrose interface visible. The membranous material at the interface was collected with a pasteur pipet and transferred into 2 clean nalgene 40 ml centrifuge tubes. Volume was brought up to 40mls with ice cold sucrose buffer. Tubes were balanced and centrifuged as before at 5900 RPM in J2-21 centrifuge. The supernatant was discarded and each pellet was resuspended in 4mls ice cold Tris buffer (10mM Tris, 1mM EDTA, pH 7.0 in ddH₂O) with a 1ml micropipet repeatedly, to ensure homogeneity of the solutions. Storage was in 50ul aliquots at -70°C in freezing vials.

The SCF radioreceptor assay was conducted as follows with all steps being performed on ice. Human SCF samples were diluted in RRA buffer (50mM Tris, 0.25% BSA pH 7.5) and added to 1.5ml eppendorf tubes up to 5 150ul total volume. 50,000 counts in 50ul buffer of ^{125}I -huSCF (provided by ICN radiochemicals) were added to each tube. A dilution of isolated OCIM1 plasma membrane in 50ul buffer known to give 20% specific binding was then added to each tube. Tubes were 10 vortexed and allowed to incubate for 24hrs at 4°C. 400ul of buffer was then added to each tube and the tubes were centrifuged for 8 minutes at 18,000 RPM in J2-21 centrifuge, JA-18.1 fixed angle (45%) rotor, 4°C. All tubes were oriented with lid opening tabs 15 straight up. Supernatants were carefully aspirated by a sliding a 21 gauge needle down the side opposite the pellet (hinge side of tube) to bottom of each tube. Tubes were counted in gamma counter for 1 min. each.

In the radioreceptor assay, human 20 $[\text{Met}^{-1}]\text{SCF}^{\text{1-164}}$ and human $[\text{Met}^{-1}]\text{SCF}^{\text{1-165}}$, prepared from E. coli as described in Example 10, compete equally well with the binding of human $[\text{Met}^{-1}][^{125}\text{I}]\text{SCF}^{\text{1-164}}$, indicating that they bind equally well to the SCF receptor.

25

EXAMPLE 10

Purification of Recombinant SCF Products Expressed in E. coli

30 A. SCF¹⁻¹⁶⁴

Fermentation of E. coli human SCF¹⁻¹⁶⁴ was performed according to Example 6C. The harvested cells (912 g wet weight) were suspended in water to a volume 35 of 4.6 L and broken by three passes through a laboratory homogenizer (Gaulin Model 15MR-8TBA) at 8000 psi. A

broken cell pellet fraction was obtained by centrifugation (17700 x g, 30 min, 4°C), washed once with water (resuspension and recentrifugation), and finally suspended in water to a volume of 400 ml.

- 5 The pellet fraction containing insoluble SCF (estimate of 10-12 g SCF) was added to 3950 ml of an appropriate mixture such that the final concentrations of components in the mixture were 8 M urea (ultrapure grade), 0.1 mM EDTA, 50 mM sodium acetate, pH 6-7; SCF
- 10 concentration was estimated as 1.5 mg/ml. Incubation was carried out at room temperature for 4 h to solubilize the SCF. Remaining insoluble material was removed by centrifugation (17700 x g, 30 min, room temperature). For refolding/reoxidation of the solubilized SCF, the
- 15 supernatant fraction was added slowly, with stirring, to 39.15 L of an appropriate mixture such that the final concentrations of components in the mixture were 2.5 M urea (ultrapure grade), 0.01 mM EDTA, 5 mM sodium acetate, 50 mM Tris-HCl pH 8.5, 1 mM glutathione, 0.02%
- 20 (wt/vol) sodium azide. SCF concentration was estimated as 150 µg/ml. After 60 h at room temperature [shorter times (e.g. -20 h) are suitable also], with stirring, the mixture was concentrated two-fold using a Millipore Pellicon ultrafiltration apparatus with three 10,000
- 25 molecular weight cutoff polysulfone membrane cassettes (15 ft² total area) and then diafiltered against 7 volumes of 20 mM Tris-HCl, pH 8. The temperature during the concentration/ultrafiltration was 4°C, pumping rate was 5 L/min, and filtration rate was 600 ml/min.
- 30 The final volume of recovered retentate was 26.5 L. By the use of SDS-PAGE carried out both with and without reduction of samples, it is evident that most (>80%) of the pellet fraction SCF is solubilized by the incubation with 8 M urea, and that after the folding/oxidation
- 35 multiple species (forms) of SCF are present, as visualized by the SDS-PAGE of unreduced samples. The

major form, which represents correctly oxidized SCF (see below), migrates with apparent M_r of about 17,000 (unreduced) relative to the molecular weight markers (reduced) described for Figure 9. Other forms include

5 material migrating with apparent M_r of about 18-20,000 (unreduced), thought to represent SCF with incorrect intrachain disulfide bonds; and bands migrating with apparent M_r s in the range of 37,000 (unreduced), or greater, thought to represent various SCF forms having

10 interchain disulfide bonds resulting in SCF polypeptide chains that are covalently linked to form dimers or larger oligomers, respectively. The following fractionation steps result in removal of remaining

E. coli contaminants and of the unwanted SCF forms, such

15 that SCF purified to apparent homogeneity, in biologically active conformation, is obtained.

The pH of the ultrafiltration retentate was adjusted to 4.5 by addition of 375 ml of 10% (vol/vol) acetic acid, leading to the presence of visible

20 precipitated material. After 60 min, at which point much of the precipitated material had settled to the bottom of the vessel, the upper 24 L were decanted and filtered through a Cuno[®] 30SP depth filter at 500 ml/min to complete the clarification. The filtrate was then

25 diluted 1.5-fold with water and applied at 4°C to an S-Sepharose Fast Flow (Pharmacia) column (9 x 18.5 cm) equilibrated in 25 mM sodium acetate, pH 4.5. The column was run at a flow rate of 5 L/h, at 4°C. After sample application, the column was washed with five column

30 volumes (~6 L) of column buffer and SCF material, which was bound to the column, was eluted with a gradient of 0 to 0.35 M NaCl in column buffer. Total gradient volume was 20 L and fractions of 200 ml were collected. The elution profile is depicted in Figure 33. Aliquots

35 (10 μ l) from fractions collected from the S-Sepharose column were analyzed by SDS-PAGE carried out both with

(Figure 32 A) and without (Figure 32 B) reduction of the samples. From such analyses it is apparent that virtually all of the absorbance at 280 nm (Figures 32 and 33) is due to SCF material.

5 The correctly oxidized form predominates in the major absorbance peak (fractions 22-38, Figure 33). Minor species (forms) which can be visualized in fractions include the incorrectly oxidized material with apparent M_r of 18-20,000 on SDS-PAGE
10 (unreduced), present in the leading shoulder of the main absorbance peak (fractions 10-21, Figure 32 B); and disulfide-linked dimer material present throughout the absorbance region (fractions 10-38, Figure 32 B).

 Fractions 22-38 from the S-Sepharose column
15 were pooled, and the pool was adjusted to pH 2.2 by addition of about 11 ml 6 N HCl and applied to a Vydac C_4 column (height 8.4 cm, diameter 9 cm) equilibrated with 50% (vol/vol) ethanol, 12.5 mM HCl (solution A) and operated at 4°C. The column resin was prepared by
20 suspending the dry resin in 80% (vol/vol) ethanol, 12.5 mM HCl (solution B) and then equilibrating it with solution A. Prior to sample application, a blank gradient from solution A to solution B (6 L total volume) was applied and the column was then re-
25 equilibrated with solution A. After sample application, the column was washed with 2.5 L of solution A and SCF material, bound to the column, was eluted with a gradient from solution A to solution B (18 L total volume) at a flow rate of 2670 ml/h. 286 fractions of
30 50 ml each were collected, and aliquots were analyzed by absorbance at 280 nm (Figure 35), and by SDS-PAGE (25 μ l per fraction) as described above (Figure 34 A; reducing conditions; Figure 34 B, nonreducing conditions).
Fractions 62-161, containing correctly oxidized SCF in a
35 highly purified state, were pooled [the relatively small amounts of incorrectly oxidized monomer with M_r of about

18-20,000 (unreduced) eluted later in the gradient (about fractions 166-211) and disulfide-linked dimer material also eluted later (about fractions 199-235) (Figure 35)].

5 To remove ethanol from the pool of fractions 62-161, and to concentrate the SCF, the following procedure utilizing Q-Sepharose Fast Flow (Pharmacia) ion exchange resin was employed. The pool (5 L) was
10 diluted with water to a volume of 15.625 L, bringing the ethanol concentration to about 20% (vol/vol). Then 1 M Tris base (135 ml) was added to bring the pH to 8, followed by 1 M Tris-HCl, pH 8, (23.6 ml) to bring the total Tris concentration to 10 mM. Next 10 mM Tris-HCl, pH 8 (~15.5 L) was added to bring the total volume to
15 31.25 L and the ethanol concentration to about 10% (vol/vol). The material was then applied at 4°C to a column of Q-Sepharose Fast Flow (height 61.5 cm, diameter 7 cm) equilibrated with 10 mM Tris-HCl, pH 8, and this was followed by washing of the column with 2.5 L of
20 column buffer. Flow rate during sample application and wash was about 5.5 L/h. To elute the bound SCF, 200 mM NaCl, 10 mM Tris-HCl, pH 8 was pumped in reverse direction through the column at about 200 ml/h. Fractions of about 12 ml were collected and analyzed by
25 absorbance at 280 nm, and SDS-PAGE as above. Fractions 16-28 were pooled (157 ml).

 The pool containing SCF was then applied in two separate chromatographic runs (78.5 ml applied for each) to a Sephacryl S-200 HR (Pharmacia) gel filtration column
30 (5 x 138 cm) equilibrated with phosphate-buffered saline at 4°C. Fractions of about 15 ml were collected at a flow rate of about 75 ml/h. In each case a major peak of material with absorbance at 280 nm eluted in fractions corresponding roughly to the elution volume range of 1370
35 to 1635 ml. The fractions representing the absorbance peaks from the two column runs were combined into a

single pool of 525 ml, containing about 2.3 g of SCF. This material was sterilized by filtration using a Millipore Millipak 20 membrane cartridge.

Alternatively, material from the C₄ column can be concentrated by ultrafiltration and the buffer exchanged by diafiltration, prior to sterile filtration.

The isolated recombinant human SCF¹⁻¹⁶⁴ material is highly pure (>98% by SDS-PAGE with silver-staining) and is considered to be of pharmaceutical grade. Using the methods outlined in Example 2, it is found that the material has amino acid composition and amino acid sequence matching those expected from analysis of the SCF gene. The N-terminal amino acid sequence is Met-Glu-Gly-Ile..., i.e., the initiating Met residue is retained.

By procedures comparable to those outlined for human SCF¹⁻¹⁶⁴ expressed in *E. coli*, rat SCF¹⁻¹⁶⁴ (also present in insoluble form inside the cell after fermentation) can be recovered in a purified state with high biological specific activity. Similarly, human SCF¹⁻¹⁸³ and rat SCF¹⁻¹⁹³ can be recovered. The rat SCF¹⁻¹⁹³, during folding/oxidation, tends to form more variously oxidized species, and the unwanted species are more difficult to remove chromatographically.

The rat SCF¹⁻¹⁹³ and human SCF¹⁻¹⁸³ are prone to proteolytic degradation during the early stages of recovery, i.e., solubilization and folding/oxidation. A primary site of proteolysis is located between residues 160 and 170. The proteolysis can be minimized by appropriate manipulation of conditions (e.g., SCF concentration; varying pH; inclusion of EDTA at 2-5 mM, or other protease inhibitors), and degraded forms to the extent that they are present can be removed by appropriate fractionation steps.

While the use of urea for solubilization, and during folding/oxidation, as outlined, is a preferred

embodiment, other solubilizing agents such as guanidine-HCl (e.g. 6 M during solubilization and 1.25 M during folding/oxidation) and sodium N-lauroyl sarcosine can be utilized effectively. Upon removal of the agents after
5 folding/oxidation, purified SCFs, as determined by SDS-PAGE, can be recovered with the use of appropriate fractionation steps.

In addition, while the use of glutathione at 1 mM during folding/oxidation is a preferred embodiment,
10 other conditions can be utilized with equal or nearly equal effectiveness. These include, for example, the use in place of 1 mM glutathione of 2 mM glutathione plus 0.2 mM oxidized glutathione, or 4 mM glutathione plus 0.4 mM oxidized glutathione, or 1 mM
15 2-mercaptoethanol, or other thiol reagents also.

In addition to the chromatographic procedures described, other procedures which are useful in the recovery of SCFs in a purified active form include hydrophobic interaction chromatography [e.g., the use of
20 phenyl-Sepharose (Pharmacia), applying the sample at neutral pH in the presence of 1.7 M ammonium sulfate and eluting with a gradient of decreasing ammonium sulfate]; immobilized metal affinity chromatography [e.g., the use of chelating-Sepharose (Pharmacia) charged with Cu^{2+}
25 ion, applying the sample at near neutral pH in the presence of 1 mM imidazole and eluting with a gradient of increasing imidazole]; hydroxylapatite chromatography, [applying the sample at neutral pH in the presence of 1 mM phosphate and eluting with a
30 gradient of increasing phosphate]; and other procedures apparent to those skilled in the art.

Other forms of human SCF, corresponding to all or part of the open reading frame encoding by amino acids 1-248 in Figure 42, or corresponding to the open
35 reading frame encoded by alternatively spliced mRNAs that may exist (such as that represented by the cDNA

sequence in Figure 44), can also be expressed in E. coli and recovered in purified form by procedures similar to those described in this Example, and by other procedures apparent to those skilled in the art.

5 The purification and formulation of forms including the so-called transmembrane region referred to in Example 16 may involve the utilization of detergents, including non-ionic detergents, and lipids, including phospholipid-containing liposome structures.

10

B. SCF¹-165

For the purification of human SCF¹-165 expressed in E. coli, the following information is
15 relevant. After harvesting of cells expressing the human SCF¹-165, pharmaceutical grade human SCF¹-165 was recovered by procedures the same as those described for human SCF¹-164 (above), but with the following modifications. After cell lysis, the homogenate was
20 diluted to a volume representing twice the volume of the original cell suspension, with the inclusion of EDTA to 10 mM final concentration. Centrifugation was then done using a Sharples AS-16 centrifuge at 15,000 rpm and flow rate of 0.5 L/min, to obtain a pellet fraction. This
25 pellet fraction, without washing, was then subjected to the solubilization with urea, essentially as described for human SCF¹-164 except that sodium acetate was omitted, the mixture was titrated to pH 3 using HCl, the estimated SCF concentration was 3.2 mg/ml, and
30 incubation was for 1-2 h at room temperature. All subsequent steps were at room temperature also. For refolding/reoxidation, the mixture was then diluted directly, by a factor of 3.2, such that the final conditions included the SCF at about 1 mg/ml, 2.5 M
35 urea, 60 mM NaCl, 1 mM glutathione, 50 mM Tris-HCl, with pH at 8.5. After stirring for 20-24 h, clarification

was accomplished by filtration through a Cuno Zeta Plus 30SP depth filtration device. A 19 ft² filter was used per 100 L of mixture to be filtered. Flow rate during filtration was about 2.9 L/min. For a 19 ft² filter, 5 washing of the filter with 50 L of 20 mM Tris-HCl, pH 8.5 was done. The following description applies to the handling of fractions derived from 100 L of refolding/reoxidation mixture. The 150 L of filtrate plus wash was concentrated to 50 L by ultrafiltration, 10 and diafiltration against 300 L of 20 mM Tris-HCl, pH 8.5 was then done. The diafiltered material was then diluted to 150 L by addition of the Tris buffer. pH was then adjusted to 4.55 using 10% acetic acid, whereupon the mixture became turbid. 2-24 h later, clarification 15 was accomplished by depth filtration using a 19 ft² Cuno Zeta Plus 10SP filter, pre-washed with 0.1 M sodium chloride, 50 mM sodium acetate, pH 4.5. After the filtration, the filter was washed with 50 L of the same sodium chloride/sodium acetate buffer. The resulting 20 filtrate plus wash (about 200 L) was applied to an S-Sepharose Fast Flow (Pharmacia) column (10 L bed volume; 30 cm diameter) equilibrated with 50 mM sodium acetate, 100 mM sodium chloride, pH 4.5. Flow rate was 1.4 L/min. After sample application, the column was washed 25 with 100 L of the column buffer, at a flow rate of 1.2 L/min. Elution was carried out with a linear gradient from the starting column buffer to 50 mM sodium acetate, 300 mM NaCl, pH 4.5 (200 L total gradient volume), at flow rate of 0.65 L/min. The various forms described 30 for the S-Sepharose Fast Flow fractions obtained in preparation of E. coli-derived human SCF¹⁻¹⁶⁴ above were present in essentially the same fashion, and pooling of fractions was based on the same criteria as described above. The pooled material (about 25 g SCF in about 35 20-25 L) was adjusted to pH 2.2 using 6 N HCl, and loaded onto a C4 column (1.2 L bed volume; 14 cm

diameter; Vydac Proteins C₄, Cat. No. 214TPB2030), at 100 ml/min. The column was next washed with 10 L of 25% ethanol, 12.5 mM HCl, and then eluted with a linear gradient from this buffer to 75% ethanol, 12.5 mM HCl (25 L total gradient volume). Again, the various species present in the eluted fractions, and the pooling of fractions, were essentially as described for the SCF¹⁻¹⁶⁴. The pool, containing about 16 g SCF¹⁻¹⁶⁵ correctly-oxidized monomer in a volume of about 9 ml, was diluted 6.25-fold, made 10 mM in sodium phosphate by addition of 0.5 M sodium phosphate, pH 6.5, and titrated to pH 6.5 using 1 N sodium hydroxide. The material was then applied at a flow rate of 400 ml/min to a Q-Sepharose Fast Flow (Pharmacia) column (2 L bed volume; 14 cm diameter) equilibrated with 10 mM sodium phosphate, pH 6.5. After washing the column with 20 L of 10 mM sodium phosphate, 25 mM sodium chloride, pH 6.5, elution was carried out with a linear gradient from the wash buffer to 10 mM sodium phosphate, 100 mM NaCl, pH 6.5. Fractions corresponding to the main absorbance (at 280 nm) peak represent the correctly-oxidized SCF¹⁻¹⁶⁵. These fractions were pooled; typically the pool contained about 12-15 g SCF¹⁻¹⁶⁵, in a volume of about 17-18 L. The SCF material was then concentrated by ultrafiltration and other buffers optionally introduced by diafiltration, a preferred buffer being 10 mM sodium acetate, 140 mM sodium chloride, pH 5.

C. SCF¹⁻²⁴⁸

30

The full length recombinant human stem cell factor (SCF¹⁻²⁴⁸) is formed in E. coli as inclusion bodies. After isolation of the inclusion bodies, treatment with 8M urea, 50 mM sodium acetate, 0.1 mM EDTA, pH 5.0 does not solubilize any SCF¹⁻²⁴⁸. This is in contrast to shorter SCFs which solubilize well in this

buffer. To solubilize SCF¹⁻²⁴⁸, the urea-washed inclusion bodies are suspended in 50 mM Tris-HCl, 1 mM EDTA, 2% sodium deoxycholate (NaDOC), pH 8.5 at an approximate SCF¹⁻²⁴⁸ concentration of 0.2 to 1.0 mg/mL.

5 To this is added powdered dithiothreitol (DTT) to a concentration of 20 mM. The mixture is stirred for 2.5 hours at room temperature. Unsolubilized debris is removed by centrifuging at 20,000 x g for 20 min. The supernatant contains all of the SCF¹⁻²⁴⁸ which runs as a

10 fuzzy 33,000 dalton band on a reducing SDS polyacrylamide gel. Both NaDOC, an anionic detergent, and DTT, a reducing agent are required for solubilization.

Soluble oxidized SCF¹⁻²⁴⁸ can be prepared by diluting the solubilization mixture supernatant with

15 nine volumes of 50 mM Tris, 1mM EDTA, 2% NaDOC (no pH adjustment). The pH of the diluted mixture is approximately 9.5. This mixture is stirred vigorously at room temperature for approximately 40 hours. This mixture can be clarified by filtration through a 0.45 μ

20 cellulose acetate membrane. The filtrate contains SCF¹⁻²⁴⁸ which runs as a 28,000 dalton band on a non-reducing SDS polyacrylamide gel. Under reducing conditions, the fuzzy 33,000 dalton band is visible. The filtrate also contains smaller but variable amounts

25 of incompletely oxidized SCF¹⁻²⁴⁸ and an apparent disulfide-linked dimer at approximately 80,000 daltons on the gels. Upon removal of NaDOC by diafiltration using a 10,000 dalton molecular weight cut-off membrane, the oxidized SCF¹⁻²⁴⁸ remains in solution.

30 SCF¹⁻²⁴⁸ was subsequently purified to 80-90% purity by a combination of anion exchange, gel filtration, and cation exchange chromatography. The protein requires the presence of the non-ionic detergent, Triton X-100, to remain unaggregated.

35 Material following anion exchange chromatography was active in the UT-7 assay (Example 9B). The final

material after cation exchange chromatography showed no activity in the UT-7 assay. It may be that earlier samples contained some active proteolyzed SCF. The SCF¹⁻²⁴⁸ diluted in detergent-free buffer for assay may be incapable of interaction with the SCF receptor because of aggregation.

EXAMPLE 11

Recombinant SCF from Mammalian Cells

10

A. Fermentation of CHO Cells Producing SCF

Recombinant Chinese hamster ovary (CHO) cells (strain CHO pDSRa2 hSCF¹⁻¹⁶²) were grown on microcarriers in a 20 liter perfusion culture system for the production of human SCF¹⁻¹⁶². The fermentor system is similar to that used for the culture of BRL 3A cells, Example 1B, except for the following: The growth medium used for the culture of CHO cells was a mixture of Dulbecco's Modified Eagle Medium (DMEM) and Ham's F-12 nutrient mixture in a 1:1 proportion (GIBCO), supplemented with 2 mM glutamine, nonessential amino acids (to double the existing concentration by using 1:100 dilution of Gibco #320-1140) and 5% fetal bovine serum. The harvest medium was identical except for the omission of serum. The reactor was inoculated with 5.6×10^9 CHO cells grown in two 3-liter spinner flasks. The cells were allowed to grow to a concentration of 4×10^5 cells/ml. At this point 100 grams of presterilized cytodex-2 microcarriers (Pharmacia) were added to the reactor as a 3-liter suspension in phosphate buffered saline. The cells were allowed to attach and grow on the microcarriers for four days. Growth medium was perfused through the reactor as needed based on glucose consumption. The glucose concentration was maintained at approximately 2.0 g/L. After four

days, the reactor was perfused with six volumes of serum-free medium to remove most of the serum (protein concentration <50 µg/ml). The reactor was then operated batch-wise until the glucose concentration fell below 2 g/L. From this point onward, the reactor was operated at a continuous perfusion rate of approximately 20 L/day. The pH of the culture was maintained at 6.9 ± 0.3 by adjusting the CO₂ flow rate. The dissolved oxygen was maintained higher than 20% of air saturation by supplementing with pure oxygen as necessary. The temperature was maintained at $37 \pm 0.5^\circ \text{C}$.

Approximately 450 liters of serum-free conditioned medium was generated from the above system and was used as starting material for the purification of recombinant human SCF¹⁻¹⁶².

Approximately 589 liters of serum-free conditioned medium was also generated in similar fashion but using strain CHO pDSR α 2 rSCF¹⁻¹⁶² and used as starting material for purification of rat SCF¹⁻¹⁶².

B. Purification of Recombinant Mammalian Expressed Rat SCF¹⁻¹⁶² and Other Recombinant Mammalian SCFs

All purification work was carried out at 4°C unless indicated otherwise.

1. Concentration and Diafiltration

Conditioned medium generated by serum-free growth of cell strain CHO pDSR α 2 rat SCF¹⁻¹⁶² as performed in Section A above, was clarified by filtration thru 0.45 µ Sartocapsules (Sartorius). Several different batches (36 L, 101 L, 102 L, 200 L and 150 L) were separately subjected to concentration and diafiltration/buffer exchange. To illustrate, the handling of the 36 L batch was as follows. The filtered condition medium was concentrated to ~500 ml using a

Millipore Pellicon tangential flow ultrafiltration apparatus with three 10,000 molecular weight cutoff cellulose acetate membrane cassettes (15 ft² total membrane area; pump rate -2,200 ml/min and filtration rate -750 ml/min). Diafiltration/buffer exchange in preparation for anion exchange chromatography was then accomplished by adding 1000 ml of 10 mM Tris-HCl, pH 6.7-6.8 to the concentrate, reconcentrating to 500 ml using the tangential flow ultrafiltration apparatus, and repeating this 5 additional times. The concentrated/diafiltered preparation was finally recovered in a volume of 1000 ml. The behavior of all conditioned medium batches subjected to the concentration and diafiltration/buffer exchange was similar. Protein concentrations for the batches, determined by the method of Bradford [Anal. Bioch. 72, 248-254 (1976)] with bovine serum albumin as standard, were in the range 70-90 µg/ml. The total volume of conditioned medium utilized for this preparation was about 589 L.

2. Q-Sepharose Fast Flow Anion Exchange Chromatography

The concentrated/diafiltered preparations from each of the five conditioned medium batches referred to above were combined (total volume 5,000 ml). pH was adjusted to 6.75 by adding 1 M HCl. 2000 ml of 10 mM Tris-HCl, pH 6.7 was used to bring conductivity to about 0.700 mmho. The preparation was applied to a Q-Sepharose Fast Flow anion exchange column (36 x 14 cm; Pharmacia Q-Sepharose Fast Flow resin) which had been equilibrated with the 10 mM Tris-HCl, pH 6.7 buffer. After sample application, the column was washed with 28,700 ml of the Tris buffer. Following this washing the column was washed with 23,000 ml of 5 mM acetic acid/1 mM glycine/6 M urea/20 µM CuSO₄ at about pH 4.5. The column was then washed with 10 mM Tris-HCl,

20 μM CuSO_4 , pH 6.7 buffer to return to neutral pH and remove urea, and a salt gradient (0-700 mM NaCl in the 10 mM Tris-HCl, 20 μM CuSO_4 , pH 6.7 buffer; 40 L total volume) was applied. Fractions of about 490 ml were
5 collected at a flow rate of about 3,250 ml/h. The chromatogram is shown in Figure 36. "MC/9 cpm" refers to biological activity in the MC/9 assay; 5 μl from the indicated fractions was assayed. Eluates collected during the sample application and washes are not shown
10 in the Figure; no biological activity was detected in these fractions.

3. Chromatography Using Silica-Bound Hydrocarbon Resin

Fractions 44-66 from the run shown in
15 Figure 36 were combined (11,200 ml) and EDTA was added to a final concentration of 1 mM. This material was applied at a flow rate of about 2000 ml/h to a C_4 column (Vydac Proteins C_4 ; 7 x 8 cm) equilibrated with buffer A (10 mM Tris pH 6.7/20% ethanol). After sample
20 application the column was washed with 1000 ml of buffer A. A linear gradient from buffer A to buffer B (10 mM Tris pH 6.7/94% ethanol) (total volume 6000 ml) was then applied, and fractions of 30-50 ml were collected. Portions of the C_4 column starting sample,
25 runthrough pool and wash pool in addition to 0.5 ml aliquots of the gradient fractions were dialyzed against phosphate-buffered saline in preparation for biological assay. These various fractions were assayed by the MC/9 assay (5 μl aliquots of the prepared gradient fractions;
30 cpm in Figure 37). SDS-PAGE [Laemmli, Nature 227, 680-685 (1970); stacking gels contained 4% (w/v) acrylamide and separating gels contained 12.5% (w/v) acrylamide] of aliquots of various fractions is shown in Figure 38. For the gels shown, sample aliquots (100 μl)
35 were dried under vacuum and then redissolved using 20 μl sample treatment buffer (reducing, i.e., with

2-mercaptoethanol) and boiled for 5 min prior to loading onto the gel. The numbered marks at the left of the Figure represent migration positions of molecular weight markers (reduced) as in Figure 6. The numbered lanes 5 represent the corresponding fractions collected during application of the last part of the gradient. The gels were silver-stained [Morrissey, Anal. Bioch. 117, 307-310 (1981)].

10 4. Q-Sepharose Fast Flow Anion Exchange Chromatography

Fractions 98-124 from the C₄ column shown in Figure 37 were pooled (1050 ml). The pool was diluted 1:1 with 10 mM Tris, pH 6.7 buffer to reduce ethanol concentration. The diluted pool was then applied to a

15 Q-Sepharose Fast Flow anion exchange column (3.2 x 3 cm, Pharmacia Q-Sepharose Fast Flow resin) which had been equilibrated with the 10 mM Tris-HCl, pH 6.7 buffer. Flow rate was 463 ml/h. After sample application the column was washed with 135 ml of column buffer and
20 elution of bound material was carried out by washing with 10 mM Tris-HCl, 350 mM NaCl, pH 6.7. The flow direction of the column was reversed in order to minimize volume of eluted material, and 7.8 ml fractions were collected during elution.

25

5. Sephacryl S-200 HR Gel Filtration Chromatography

Fractions containing eluted protein from the salt wash of the Q-Sepharose Fast Flow anion exchange column were pooled (31 ml). 30 ml was applied to a
30 Sephacryl S-200 HR (Pharmacia) gel filtration column, (5 x 55.5 cm) equilibrated in phosphate-buffered saline. Fractions of 6.8 ml were collected at a flow rate of 68 ml/hr. Fractions corresponding to the peak of absorbance at 280 nm were pooled and represent the
35 final purified material.

Table 15 shows a summary of the purification.

TABLE 15.

5 Summary of Purification of Mammalian Expressed Rat SCF¹⁻¹⁶²

Step	Volume(ml)	Total
		Protein (mg)*
Conditioned medium (concentrated)	7,000	28,420
10 Q-Sepharose Fast Flow	11,200	974
C ₄ resin	1,050	19
Q-Sepharose Fast Flow	31	20
Sephacryl S-200 HR	82	19**

*Determined by the method of Bradford (supra, 1976).

15 **Determined as 47.3 mg by quantitative amino acid analysis using methodology similar to that outlined in Example 2.

 The N-terminal amino acid sequence of purified rat SCF¹⁻¹⁶² is approximately half Gln-Glu-Ile... and
 20 half PyroGlu-Glu-Ile..., as determined by the methods outlined in Example 2. This result indicates that rat SCF¹⁻¹⁶² is the product of proteolytic processing/cleavage between the residues indicated as numbers (-1) (Thr) and (+1) (Gln) in Figure 14C.
 25 Similarly, purified human SCF¹⁻¹⁶² from transfected CHO cell conditioned medium (below) has N-terminal amino acid sequence Glu-Gly-Ile, indicating that it is the product of processing/cleavage between residues indicated as numbers (-1) (Thr) and (+1) (Glu) in
 30 Figure 15C.

 Using the above-described protocol will yield purified human SCF protein, either recombinant forms expressed in CHO cells or naturally derived.

 Additional purification methods that are of
 35 utility in the purification of mammalian cell derived recombinant SCFs include those outlined in Examples 1

and 10, and other methods apparent to those skilled in the art.

Other forms of human SCF, corresponding to all or part of the open reading frame encoded by amino acids 1-248 shown in Figure 42, or corresponding to the open reading frame encoded by alternatively spliced mRNAs that may exist (such as that represented by the cDNA sequence in Figure 44), can also be expressed in mammalian cells and recovered in purified form by procedures similar to those described in this Example, and by other procedures apparent to those skilled in the art.

C. SDS-PAGE and Glycosidase Treatments

15

SDS-PAGE of pooled fractions from the Sephacryl S-200 HR gel filtration column is shown in Figure 39; 2.5 μ l of the pool was loaded (lane 1). The lane was silver-stained. Molecular weight markers (lane 6) were as described for Figure 6. The different migrating material above and slightly below the M_r 31,000 marker position represents the biologically active material; the apparent heterogeneity is largely due to the heterogeneity in glycosylation.

25

To characterize the glycosylation purified material was treated with a variety of glycosidases, analyzed by SDS-PAGE (reducing conditions) and visualized by silver-staining. Results are shown in Figure 39. Lane 2, neuraminidase. Lane 3, neuraminidase and O-glycanase. Lane 4, neuraminidase, O-glycanase and N-glycanase. Lane 5, neuraminidase and N-glycanase. Lane 7, N-glycanase. Lane 8, N-glycanase without substrate. Lane 9, O-glycanase without substrate. Conditions were 10 mM 3-[(3-cholamidopropyl) dimethyl ammonio]-1-propane sulfonate (CHAPS), 66.6 mM 2-mercaptoethanol, 0.04% (wt/vol) sodium azide, phosphate buffered saline, for 30 min at 37°C, followed

30

35

by incubation at half of described concentrations in presence of glycosidases for 18 h at 37°C.

Neuraminidase (from Arthrobacter ureafaciens; supplied by Calbiochem) was used at 0.5 units/ml final

- 5 concentration. O-Glycanase (Genzyme; endo-alpha-N-acetyl galactosaminidase) was used at 7.5 milliunits/ml. N-Glycanase (Genzyme; peptide: N-glycosidase F; peptide-N⁴[N-acetyl-beta-glucosaminyl] asparagine amidase) was used at 10 units/ml.

- 10 Where appropriate, various control incubations were carried out. These included: incubation without glycosidases, to verify that results were due to the glycosidase preparations added; incubation with glycosylated proteins (e.g. glycosylated recombinant
15 human erythropoietin) known to be substrates for the glycosidases, to verify that the glycosidase enzymes used were active; and incubation with glycosidases but no substrate, to judge where the glycosidase preparations were contributing to or obscuring the
20 visualized gel bands (Figure 39, lanes 8 and 9).

- A number of conclusions can be drawn from the experiments described above. The various treatments with N-glycanase [which removes both complex and high-mannose N-linked carbohydrate (Tarentino et al.,
25 Biochemistry 24, 4665-4671 (1988)], neuraminidase (which removes sialic acid residues), and O-glycanase [which removes certain O-linked carbohydrates (Lambin et al., Biochem. Soc. Trans. 12, 599-600 (1984)], suggest that: both N-linked and O-linked carbohydrates are
30 present; and sialic acid is present, with at least some of it being part of the O-linked moieties. The fact that treatment with N-glycanase can convert the heterogeneous material apparent by SDS-PAGE to a faster-migrating form which is much more homogeneous indicates
35 that all of the material represents the same polypeptide, with the heterogeneity being caused mainly by heterogeneity in glycosylation.

While the results of this section apply to purified CHO cell-derived rat SCF¹⁻¹⁶², equivalent results of SDS-PAGE and glycosidase treatments are obtained for CHO cell-derived human SCF¹⁻¹⁶².

5

EXAMPLE 12

Preparation of Recombinant SCF PEG

A. Preparation of Recombinant SCF¹⁻¹⁶⁴ PEG

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Rat SCF¹⁻¹⁶⁴, purified from a recombinant E. coli expression system according to Examples 6A and 10, was used as starting material for polyethylene glycol modification described below.

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Methoxypolyethylene glycol-succinimidyl succinate (18.1 mg = 3.63 μ mol; SS-MPEG = Sigma Chemical Co. no. M3152, approximate molecular weight = 5,000) in 0.327 mL deionized water was added to 13.3 mg (0.727 μ mol) recombinant rat SCF¹⁻¹⁶⁴ in 1.0 mL 138 mM sodium phosphate, 62 mM NaCl, 0.62 mM sodium acetate, pH 8.0. The resulting solution was shaken gently (100 rpm) at room temperature for 30 minutes. A 1.0 mL aliquot of the final reaction mixture (10 mg protein) was then applied to a Pharmacia Superdex 75 gel filtration column (1.6 x 50 cm) and eluted with 100 mM sodium phosphate, pH 6.9, at a rate of 0.25 mL/min at room temperature. The first 10 mL of column effluent were discarded, and 1.0 mL fractions were collected thereafter. The UV absorbance (280 nm) of the column effluent was monitored continuously and is shown in Figure 40A. Fractions number 25 through 27 were combined and sterilized by ultrafiltration through a 0.2 μ polysulfone membrane (Gelman Sciences no. 4454), and the resulting pool was designated PEG-25. Likewise, fractions number 28 through 32 were combined, sterilized by ultrafiltration, and designated PEG-32. Pooled fraction PEG-25 contained

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3.06 mg protein and pooled fraction PEG-32 contained 3.55 mg protein, as calculated from A280 measurements using for calibration an absorbance of 0.66 for a 1.0 mg/mL solution of unmodified rat SCF¹⁻¹⁶⁴. Unreacted
5 rat SCF¹⁻¹⁶⁴, representing 11.8% of the total protein in the reaction mixture, was eluted in fractions number 34 to 37. Under similar chromatographic conditions, unmodified rat SCF¹⁻¹⁶⁴ was eluted as a major peak with a retention volume of 45.6 mL, Figure 40B. Fractions
10 number 77 to 80 in Figure 40A contained N-hydroxysuccinimide, a by-product of the reaction of rat SCF¹⁻¹⁶⁴ with SS-MPEG.

Potentially reactive amino groups in rat SCF¹⁻¹⁶⁴ include 12 lysine residues and the alpha amino
15 group of the N-terminal glutamine residue. Pooled fraction PEG-25 contained 9.3 mol of reactive amino groups per mol of protein, as determined by spectroscopic titration with trinitrobenzene sulfonic acid (TNBS) using the method described by Habeeb, Anal.
20 Biochem. 14:328-336 (1966). Likewise, pooled fraction PEG-32 contained 10.4 mol and unmodified rat SCF¹⁻¹⁶⁴ contained 13.7 mol of reactive amino groups per mol of protein, respectively. Thus, an average of 3.3 (13.7 minus 10.4) amino groups of rat SCF¹⁻¹⁶⁴ in pooled
25 fraction PEG-32 were modified by reaction with SS-MPEG. Similarly, an average of 4.4 amino groups of rat SCF¹⁻¹⁶⁴ in pooled fraction PEG-25 were modified. Human SCF (hSCF¹⁻¹⁶⁴) produced as in Example 10 was also modified using the procedures noted above.
30 Specifically, 714 mg (38.5 umol) hSCF¹⁻¹⁶⁴ were reacted with 962.5 mg (192.5 umol) SS-MPEG in 75 mL of 0.1 M sodium phosphate buffer, pH 8.0 for 30 minutes at room temperature. The reaction mixture was applied to a Sephacryl S-200HR column (5 x 134 cm) and eluted with
35 PBS (Gibco Dulbecco's phosphate-buffered saline without CaCl₂ and MgCl₂) at a rate of 102 mL/hr, and 14.3-mL

fractions were collected. Fractions no. 39-53, analogous to the PEG-25 pool described above and in Figure 40A, were pooled and found to contain a total of 354 mg of protein. In vivo activity of this modified SCF in primates is presented in Example 8C.

B. Preparation of Recombinant SCF¹⁻¹⁶⁵PEG

Recombinant human SCF¹⁻¹⁶⁵ produced as in Example 10 was coupled to methoxypolyethylene glycol (MW = 6,000) by reacting 334 mg (18.0 μ mol) of rhuSCF¹⁶⁵ with 433 mg (72.2 μ mol) of the N-hydroxysuccinimidyl ester of carboxymethyl-MPEG [prepared by procedures described by Veronese, F. M., et al., J. Controlled Release, 10:145-154 (1989) in 33.4 ml of 0.1 M bicine buffer, pH 8.0 for 1 hour at room temperature. The reaction mixture was diluted with 134 ml of water for injection (WFI), titrated to pH 4.0 with 0.5 N HCl, filtered through a 0.20 μ cellulose acetate filter (Nalgene no. 156-4020), and applied at a rate of 5.0 ml/min to a 2.6 x 19.5 cm column of S-Sepharose FF (Pharmacia) which had been previously equilibrated with 20 mM sodium acetate, pH 4.0 at room temperature. Effluent from the column was collected in 8.0-ml fractions (no. 1-18) during sample loading, and the ultraviolet absorbance (A_{280}) of the effluent was monitored continuously. The column was then sequentially washed with 200 ml of the equilibration buffer at 5.0 ml/min (fractions no. 19-44), with 200 ml of 20 mM sodium acetate, 0.5 M NaCl, pH 4.0 at 8.0 ml/min (fractions no. 45-69), and finally with 200 ml of 20 mM sodium acetate, 1.0 M NaCl, pH 4.0 at 8.0 ml/min (fractions no. 70-94). Fractions (no. 28-31 and 55-62) containing MPEG-rhu-SCF¹⁻¹⁶⁵ were combined and dialyzed by ultrafiltration (Amicon YM-10 membrane) against 10 mM sodium acetate, 140 mM NaCl, pH 5.0 to yield 284 mg of

final product in a volume of 105 ml. The resulting MPEG-rhu-SCF¹⁶⁵ was shown to be free of unbound MPEG and other reaction by-products by analytical size-exclusion HPLC [Toso-Haas TSK G3000 SWXL and G4000 SWXL columns (each 0.68 x 30 cm; 5 u) connected in tandem; 0.1 M sodium phosphate, pH 6.9 at 1.0 ml/min at room temperature; UV absorbance (280 nm) and refractive index detectors in series].

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EXAMPLE 13

SCF Receptor Expression on Leukemic Blasts

Leukemic blasts were harvested from the peripheral blood of a patient with a mixed lineage leukemia. The cells were purified by density gradient centrifugation and adherence depletion. Human SCF¹⁻¹⁶⁴ was iodinated according to the protocol in Example 7. The cells were incubated with different concentrations of iodinated SCF as described [Broudy, Blood, 75 1622-1626 (1990)]. The results of the receptor binding experiment are shown in Figure 41. The receptor density estimated is approximately 70,000 receptors/cell.

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EXAMPLE 14

Rat SCF Activity on Early Lymphoid Precursors

The ability of recombinant rat SCF¹⁻¹⁶⁴ (rrSCF¹⁻¹⁶⁴), to act synergistically with IL-7 to enhance lymphoid cell proliferation was studied in agar cultures of mouse bone marrow. In this assay, the colonies formed with rrSCF¹⁻¹⁶⁴ alone contained monocytes, neutrophils, and blast cells, while the colonies stimulated by IL-7 alone or in combination with rrSCF¹⁻¹⁶⁴ contained primarily pre-B cells. Pre-B cells, characterized as B220⁺, sIg⁻, cu⁺, were identified by FACS analysis of pooled cells using

fluorescence-labeled antibodies to the B220 antigen [Coffman, Immunol. Rev., 69, 5 (1982)] and to surface Ig (FITC-goat anti-K, Southern Biotechnology Assoc., Birmingham, AL); and by analysis of cytospin slides for cytoplasmic μ expression using fluorescence-labeled antibodies (TRITC-goat anti- μ , Southern Biotechnology Assoc.,). Recombinant human IL-7 (rhIL-7) was obtained from Biosource International (Westlake Village, CA). When rrSCF¹⁻¹⁶⁴ was added in combination with the pre-B cell growth factor IL-7, a synergistic increase in colony formation was observed (Table 16), indicating a stimulatory role of rrSCF¹⁻¹⁶⁴ on early B cell progenitors.

Table 16. Stimulation of Pre-B Cell Colony Formation by rrSCF¹⁻¹⁶⁴ in Combination with hIL-7

Growth Factors		Colony Number ¹
20	Saline	0
	rrSCF ¹⁻¹⁶⁴ 200 ng	13 \pm 2
	100 ng	7 \pm 4
	50 ng	4 \pm 2
	rhIL-7 200 ng	21 \pm 6
25	100 ng	18 \pm 6
	50 ng	13 \pm 6
	25 ng	4 \pm 2
	rhIL-7 200 ng + rrSCF ¹⁻¹⁶⁴ 200 ng	60 \pm 0
	100 ng + 200 ng	48 \pm 8
30	50 ng + 200 ng	24 \pm 10
	25 ng + 200 ng	21 \pm 2

¹ Number of colonies per 5×10^4 mouse bone marrow cells plated.

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Each value is the mean of triplicate dishes \pm SD.

EXAMPLE 15

Identification of the Receptor for SCF

A. c-kit is the Receptor for SCF¹⁻¹⁶⁴

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To test whether SCF¹⁻¹⁶⁴ is the ligand for c-kit, the cDNA for the entire murine c-kit [Qiu et al., EMBO J., 7, 1003-1011 (1988)] was amplified using PCR from the SCF¹⁻¹⁶⁴ responsive mast cell line MC/9 [Nabel et al., Nature, 291, 332-334 (1981)] with primers designed from the published sequence. The ligand binding and transmembrane domains of human c-kit, encoded by amino acids 1-549 [Yarden et al., EMBO J., 6, 3341-3351 (1987)], were cloned using similar techniques from the human erythroleukemia cell line, HEL [Martin and Papayannopoulou, Science, 216, 1233-1235 (1982)]. The c-kit cDNAs were inserted into the mammalian expression vector V19.8 transfected into COS-1 cells, and membrane fractions prepared for binding assays using either rat or human ¹²⁵I-SCF¹⁻¹⁶⁴ according to the methods described in Sections B and C below. Table 17 shows the data from a typical binding assay. There was no detectable specific binding of ¹²⁵I human SCF¹⁻¹⁶⁴ to COS-1 cells transfected with V19.8 alone. However, COS-1 cells expressing human recombinant c-kit ligand binding plus transmembrane domains (hckit-LT1) did bind ¹²⁵I-hSCF¹⁻¹⁶⁴ (Table 17). The addition of a 200 fold molar excess of unlabelled human SCF¹⁻¹⁶⁴ reduced binding to background levels. Similarly, COS-1 cells transfected with the full length murine c-kit (mckit-L1) bound rat ¹²⁵I-SCF¹⁻¹⁶⁴. A small amount of rat ¹²⁵I-SCF¹⁻¹⁶⁴ binding was detected in COS-1 cells transfectants with V19.8 alone, and has also been observed in untransfected cells (not shown), indicating that COS-1 cells express endogenous c-kit. This finding is in accord with the broad cellular distribution of

c-kit expression. Rat ^{125}I -SCF¹⁻¹⁶⁴ binds similarly to both human and murine c-kit, while human ^{125}I -SCF¹⁻¹⁶⁴ bind with lower activity to murine c-kit (Table 17). This data is consistent with the pattern of SCF¹⁻¹⁶⁴ cross-reactivity between species. Rat SCF¹⁻¹⁶⁴ induces proliferation of human bone marrow with a specific activity similar to that of human SCF¹⁻¹⁶⁴, while human SCF¹⁻¹⁶⁴ induced proliferation of murine mast cells occurs with a specific activity 800 fold less than the rat protein.

In summary, these findings confirm that the phenotypic abnormalities expressed by W or S1 mutant mice are the consequences of primary defects in c-kit receptor/ligand interactions which are critical for the development of diverse cell types.

Table 17
SCF¹⁻¹⁶⁴ Binding to Recombinant
c-kit Expressed in COS-1 Cells

Plasmid Transfected	CPM Bound ^a			
	Human SCF ¹⁻¹⁶⁴		Rat SCF ¹⁻¹⁶⁴	
	^{125}I -SCF ^b	^{125}I -SCF+cold ^c	^{125}I -SCF ^d	^{125}I -SCF+cold ^e
V19.8	2,160	2,150	1,100	550
V19.8:hckit-LT1	59,350	2,380	70,000	1,100
V19.8:mckit-L1	9,500	1,100	52,700	600

^a The average of duplicate measurements is shown; the experiment has been independently performed with similar results three times.

^b 1.6 nM human ^{125}I -SCF¹⁻¹⁶⁴

^c 1.6 nM human ^{125}I -SCF¹⁻¹⁶⁴ + 320 nM unlabelled human SCF¹⁻¹⁶⁴

^d 1.6 nM rat ^{125}I -SCF¹⁻¹⁶⁴

^e 1.6 nM rat ^{125}I -SCF¹⁻¹⁶⁴ + 320 nM unlabelled rat SCF¹⁻¹⁶⁴

B. Recombinant c-kit Expression in COS-1 Cells

Human and murine c-kit cDNA clones were derived using PCR techniques [Saiki et al., Science, 5 239, 487-491 (1988)] from total RNA isolated by an acid phenol/chloroform extraction procedure [Chomczynsky and Sacchi, Anal. Biochem., 162, 156-159, (1987)] from the human erythroleukemia cell line HEL and MC/9 cells, respectively. Unique sequence oligonucleotides were 10 designed from the published human and murine c-kit sequences. First strand cDNA was synthesized from the total RNA according to the protocol provided with the enzyme, Mo-MLV reverse transcription (Bethesda Research Laboratories, Bethesda, MD), using c-kit antisense 15 oligonucleotides as primers. Amplification of overlapping regions of the c-kit ligand binding and tyrosine kinase domains was accomplished using appropriate pairs of c-kit primers. These regions were cloned into the mammalian expression vector V19.8 20 (Figure 17) for expression in COS-1 cells. DNA sequencing of several clones revealed independent mutations, presumably arising during PCR amplification, in every clone. A clone free of these mutations was constructed by reassembly of mutation-free restriction 25 fragments from separate clones. Some differences from the published sequence appeared in all or in about half of the clones; these were concluded to be the actual sequences present in the cell lines used, and may represent allelic differences from the published 30 sequences. The following plasmids were constructed in V19.8: V19.8:mckit-LT1, the entire murine c-kit; and V19.8:hckit-L1, containing the ligand binding plus transmembrane region (amino acids 1-549) of human c-kit.

The plasmids were transfected into COS-1 cells 35 essentially as described in Example 4.

C. ^{125}I -SCF¹⁻¹⁶⁴ Binding to COS-1 Cells Expressing Recombinant c-kit

Two days after transfection, the COS-1 cells
5 were scraped from the dish, washed in PBS, and frozen
until use. After thawing, the cells were resuspended in
10 mM Tris-HCl, 1 mM MgCl₂ containing 1 mM PMSF,
100 µg/ml aprotinin, 25 µg/ml leupeptin, 2 µg/ml
pepstatin, and 200 µg/ml TLCK-HCl. The suspension was
10 dispersed by pipetting up and down 5 times, incubated on
ice for 15 minutes, and the cells were homogenized with
15-20 strokes of a Dounce homogenizer. Sucrose (250mM)
was added to the homogenate, and the nuclear fraction and
residual undisrupted cells were pelleted by
15 centrifugation at 500 x g for 5 min. The supernatant was
centrifuged at 25,000 g for 30 min. at 4°C to pellet the
remaining cellular debris. Human and rat SCF¹⁻¹⁶⁴ were
radioiodinated using chloramine-T [Hunter and Greenwood,
Nature, 194, 495-496 (1962)]. COS-1 membrane fractions
20 were incubated with either human or rat ^{125}I -SCF¹⁻¹⁶⁴
(1.6nM) with or without a 200 fold molar excess of
unlabelled SCF¹⁻¹⁶⁴ in binding buffer consisting of RPMI
supplemented with 1% bovine serum albumin and 50 mM HEPES
(pH 7.4) for 1 h at 22°C. At the conclusion of the
25 binding incubation, the membrane preparations were gently
layered onto 150 µl of phthalate oil and centrifuged for
20 minutes in a Beckman Microfuge 11 to separate membrane
bound ^{125}I -SCF¹⁻¹⁶⁴ from free ^{125}I -SCF¹⁻¹⁶⁴. The pellets
were clipped off and membrane associated ^{125}I -SCF¹⁻¹⁶⁴
30 was quantitated.

EXAMPLE 16

Isolation of a Human SCF cDNA

A. Construction of the HT-1080 cDNA Library

5 Total RNA was isolated from human fibrosarcoma
cell line HT-1080 (ATCC CCL 121) by the acid guanidinium
thiocyanate-phenol-chloroform extraction method
[Chomczynski et al., Anal. Biochem. 162, 156 (1987)],
10 and poly(A) RNA was recovered by using oligo(dT) spin
column purchased from Clontech. Double-stranded cDNA
was prepared from 2 µg poly(A) RNA with a BRL (Bethesda
Research Laboratory) cDNA synthesis kit under the
conditions recommended by the supplier. Approximately
15 100ng of column fractionated double-stranded cDNA with
an average size of 2kb was ligated to 300ng SalI/NotI
digested vector pSPORT 1 [D'Alessio et al., Focus, 12,
47-50 (1990)] and transformed into DH5α (BRL, Bethesda,
MD) cells by electroporation [Dower et al., Nucl. Acids
20 Res., 16, 6127-6145 (1988)].

B. Screening of the cDNA Library

 Approximately 2.2×10^5 primary transformants
25 were divided into 44 pools with each containing ~5000
individual clones. Plasmid DNA was prepared from each
pool by the CTAB-DNA precipitation method as described
[Del Sal et al., Biotechniques, 7, 514-519 (1989)]. Two
micrograms of each plasmid DNA pool was digested with
30 restriction enzyme NotI and separated by gel
electrophoresis. Linearized DNA was transferred onto
GeneScreen Plus membrane (DuPont) and hybridized with
 ^{32}P -labeled PCR generated human SCF cDNA (Example 3)
under conditions previously described [Lin et al., Proc.
35 Natl. Acad. Sci. USA, 82, 7580-7584 (1985)]. Three
pools containing positive signal were identified from

the hybridization. These pools of colonies were rescreened by the colony-hybridization procedure [Lin et al., Gene 44, 201-209 (1986)] until a single colony was obtained from each pool. The cDNA sizes of these
5 three isolated clones are between 5.0 to 5.4 kb. Restriction enzyme digestions and nucleotide sequence determination at the 5' end indicate that two out of the three clones are identical (10-1a and 21-7a). They both contain the coding region and approximately 200bp of 5'
10 untranslated region (5'UTR). The third clone (26-1a) is roughly 400bp shorter at the 5' end than the other two clones. The sequence of this human SCF cDNA is shown in Figure 42. Of particular note is the hydrophobic transmembrane domain sequence starting in the region of
15 amino acids 186-190 and ending at amino acid 212.

C. Construction of pDSR α 2 hSCF¹⁻²⁴⁸

pDSR α 2 hSCF¹⁻²⁴⁸ was generated using plasmids
20 10-1a (as described in Example 16B) and pGEM3 hSCF¹⁻¹⁶⁴ as follows: The HindIII insert from pGEM3 hSCF¹⁻¹⁶⁴ was transferred to M13mp18. The nucleotides immediately upstream of the ATG initiation codon were changed by site directed mutagenesis from tttccttATG to
25 gccgccgccATG using the antisense oligonucleotide
5'-TCT TCT TCA TGG CGG CGG CAA GCT T 3'
and the oligonucleotide-directed in vitro mutagenesis system kit and protocols from Amersham Corp. to generate M13mp18 hSCF^{K1-164}. This DNA was digested
30 with HindIII and inserted into pDSR α 2 which had been digested with HindIII. This clone is designated pDSR α 2 hSCF^{K1-164}. DNA from pDSR α 2 hSCF^{K1-164} was digested with XbaI and the DNA made blunt ended by the addition
of Klenow enzyme and four dNTPs. Following termination
35 of this reaction the DNA was further digested with the enzyme SpeI. Clone 10-1a was digested with DraI to

generate a blunt end 3' to the open reading frame in the insert and with SpeI which cuts at the same site within the gene in both pDSR α 2 hSCF^{K1-164} and 10-1a. These DNAs were ligated together to generate pDSR α 2 hSCF^{K1-248}.

D. Transfection and immunoprecipitation of COS cells with pDSR α 2 hSCF¹⁻²⁴⁸ DNA.

COS-7 (ATCC CRL 1651) cells were transfected with DNA constructed as described above. 4×10^6 cells in 0.8 ml DMEM + 5% FBS were electroporated at 1600 V with either 10 μ g pDSR α 2 hSCF^{K1-248} DNA or 10 μ g pDSR α 2 vector DNA (vector control). Following electroporation, cells were replated into two 60-mm dishes. After 24 hrs, the medium was replaced with fresh complete medium.

72 hrs after transfection, each dish was labelled with ³⁵S-medium according to a modification of the protocol of Yarden et al. (PNAS 87, 2569-2573, 1990). Cells were washed once with PBS and then incubated with methionine-free, cysteine-free DMEM (met⁻cys⁻DMEM) for 30 min. The medium was removed and 1 ml met⁻cys⁻ DMEM containing 100 μ Ci/ml Tran³⁵S-Label (ICN) was added to each dish. Cells were incubated at 37°C for 8 hr. The medium was harvested, clarified by centrifugation to remove cell debris and frozen at -20°C.

Aliquots of labelled conditioned medium of COS/pDSR α 2 hSCF^{K1-248} and COS/pDSR α 2 vector control were immunoprecipitated along with medium samples of ³⁵S-labelled CHO/pDSR α 2 hSCF¹⁻¹⁶⁴ clone 17 cells (see Example 5) according to a modification of the protocol of Yarden et al. (EMBO, J., 6, 3341-3351, 1987). One ml of each sample of conditioned medium was treated with 10 μ l of pre-immune rabbit serum (#1379 P.I.). Samples were incubated for 5 h. at 4°C. One hundred microliters

of a 10% suspension of Staphylococcus aureus (Pansorbin, Calbiochem.) in 0.15 M NaCl, 20 mM Tris pH 7.5, 0.2% Triton X-100 was added to each tube. Samples were incubated for an additional one hour at 4°C. Immune
5 complexes were pelleted by centrifugation at 13,000 x g for 5 min. Supernatants were transferred to new tubes and incubated with 5 µl rabbit polyclonal antiserum (#1381 TB4), purified as in Example 11, against CHO derived hSCF¹⁻¹⁶² overnight at 4°C. 100 µl Pansorbin
10 was added for 1 h. and immune complexes were pelleted as before. Pellets were washed 1x with lysis buffer (0.5% Na-deoxycholate, 0.5% NP-40, 50mM NaCl, 25 mM Tris pH 8), 3x with wash buffer (0.5 M NaCl, 20 mM Tris pH 7.5, 0.2% Triton X-100), and 1x with 20 mM Tris
15 pH 7.5. Pellets were resuspended in 50 µl 10 mM Tris pH 7.5, 0.1% SDS, 0.1 M β-mercaptoethanol. SCF protein was eluted by boiling for 5 min. Samples were centrifuged at 13,000 x g for 5 min. and supernatants were recovered.
20 Treatment with glycosidases was accomplished as follows: three microliters of 75 mM CHAPS containing 1.6 mU O-glycanase, 0.5 U N-glycanase, and 0.02 U neuraminidase was added to 25 µl of immune complex samples and incubated for 3 hr. at 37°C. An equal
25 volume of 2xPAGE sample buffer was added and samples were boiled for 3 min. Digested and undigested samples were electrophoresed on a 15% SDS-polyacrylamide reducing gel overnight at 8 mA. The gel was fixed in methanol-acetic acid, treated with Enlightening enhancer
30 (NEN) for 30 min., dried, and exposed to Kodak XAR-5 film at -70°.

Figure 43 shows the autoradiograph of the results. Lanes 1 and 2 are samples from control COS/pDSRα2 cultures, lanes 3 and 4 from
35 COS/pSRα2hSCF¹⁻²⁴⁸, lanes 5 and 6 from CHO/pDSRα2 hSCF¹⁻¹⁶⁴. Lanes 1, 3, and 5 are undigested immune

precipitates; lanes 2, 4, and 6 have been digested with glycanases as described above. The positions of the molecular weight markers are shown on the left.

Processing of the SCF in COS transfected with pDSRa2 hSCF¹⁻²⁴⁸ closely resembles that of hSCF¹⁻¹⁶⁴ secreted from CHO transfected with pDSRa2 hSCF¹⁻¹⁶⁴, (Example 11). This strongly suggests that the natural proteolytic processing site releasing SCF from the cell is in the vicinity of amino acid 164.

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EXAMPLE 17

Quaternary Structure Analysis of Human SCF.

Upon calibration of the gel filtration column (ACA 54) described in Example 1 for purification of SCF from BRL cell medium with molecular weight standards, and upon elution of purified SCF from other calibrated gel filtration columns, it is evident that SCF purified from BRL cell medium behaves with an apparent molecular weight of approximately 70,000-90,000 relative to the molecular weight standards. In contrast, the apparent molecular weight by SDS-PAGE is approximately 28,000-35,000. While it is recognized that glycosylated proteins may behave anomalously in such analyses, the results suggest that the BRL-derived, rat SCF may exist as non-covalently associated dimer under non-denaturing conditions. Similar results apply for recombinant SCF forms (e.g. rat and human SCF¹⁻¹⁶⁴ derived from E. coli, rat and human SCF¹⁻¹⁶² derived from CHO cells) in that the molecular size estimated by gel filtration under non-denaturing conditions is roughly twice that estimated by gel filtration under denaturing conditions (i.e., presence of SDS), or by SDS-PAGE, in each particular case. Furthermore sedimentation velocity analysis, which provides an accurate determination of molecular weight in solution, gives a value of about

36,000 for molecular weight of E. coli-derived recombinant human SCF¹⁻¹⁶⁴. This value is again approximately twice that seen by SDS-PAGE (~18,000-19,000). Therefore, while it is recognized that there
5 may be multiple oligomeric states (including the monomeric state), it appears that the dimeric state predominates under some circumstances in solution. CHO cell-derived human SCF¹⁻¹⁶² has a molecular weight of about 53,000 by sedimentation equilibrium analysis; this
10 indicates that it is dimeric also, and that it is about 30% carbohydrate by weight.

EXAMPLE 18

Isolation of Human SCF cDNA Clones 15 from the 5637 Cell Line

A. Construction of the 5637 cDNA Library

Total RNA was isolated from human bladder
20 carcinoma cell line 5637 (ATCC HTB-9) by the acid guanidinium thiocyanate-phenol-chloroform extraction method [Chomczynski et al., Anal. Biochem, 162, 156 (1987)], and poly(A) RNA was recovered by using an oligo(dT) spin column purchased from Clontech. Double-
25 stranded cDNA was prepared from 2 µg poly(A) RNA with a BRL cDNA synthesis kit under the conditions recommended by the supplier. Approximately 80 ng of column fractionated double-stranded cDNA with an average size of 2 kb was ligated to 300 ng SalI/NotI digested vector
30 pSPORT 1 [D'Alessio et al., Focus, 12, 47-50 (1990)] and transformed into DH5a cells by electroporation [Dower et al., Nucl. Acids Res., 16, 6127-6145 (1988)].

B. Screening of the cDNA Library

Approximately 1.5×10^5 primary transformants were divided into 30 pools with each containing approximately 5000 individual clones. Plasmid DNA was prepared from each pool by the CTAB-DNA precipitation method as described [Del Sal et al., Biotechniques, 7, 514-519 (1989)]. Two micrograms of each plasmid DNA pool was digested with restriction enzyme NotI and separated by gel electrophoresis. Linearized DNA was transferred to GeneScreen Plus membrane (DuPont) and hybridized with ^{32}P -labeled full length human SCF cDNA isolated from HT1080 cell line (Example 16) under the conditions previously described [Lin et al., Proc. Natl. Acad. Sci. USA, 82, 7580-7584 (1985)]. Seven pools containing positive signal were identified from the hybridization. The pools of colonies were rescreened with ^{32}P -labeled PCR generated human SCF cDNA (Example 3) by the colony hybridization procedure [Lin et al., Gene, 44, 201-209 (1986)] until a single colony was obtained from four of the pools. The insert sizes of four isolated clones are approximately 5.3 kb. Restriction enzyme digestions and nucleotide sequence analysis of the 5'-ends of the clones indicate that the four clones are identical. The sequence of this human cDNA is shown in Figure 44. The cDNA of Figure 44 codes for a polypeptide in which amino acids 149-177 of the sequences in Figure 42 are replaced by a single Gly residue.

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EXAMPLE 19
SCF Enhancement of Survival
After Lethal Irradiation.

5 A. SCF in vivo activity on Survival After Lethal
Irradiation.

10 The effect of SCF on survival of mice after
lethal irradiation was tested. Mice used were 10 to 12
week-old female Balb/c. Groups of 5 mice were used in
all experiments and the mice were matched for body
weight within each experiment. Mice were irradiated at
850 rad or 950 rad in a single dose. Mice were injected
with factors alone or factors plus normal Balb/c bone
15 marrow cells. In the first case, mice were injected
intravenously 24 hrs. after irradiation with rat PEG-
SCF¹⁻¹⁶⁴ (20 µg/kg), purified from E. coli and modified
by the addition of polyethylene glycol as in Example 12,
or with saline for control animals. For the transplant
20 model, mice were injected i.v. with various cell doses
of normal Balb/c bone marrow 4 hours after
irradiation. Treatment with rat PEG-SCF¹⁻¹⁶⁴ was
performed by adding 200 µg/kg of rat PEG-SCF¹⁻¹⁶⁴ to the
cell suspension 1 hour prior to injection and given as a
25 single i.v. injection of factor plus cells.

After irradiation at 850 rads, mice were
injected with rat PEG-SCF¹⁻¹⁶⁴ or saline. The results
are shown in Figure 45. Injection of rat PEG-SCF¹⁻¹⁶⁴
significantly enhanced the survival time of mice
30 compared to control animals ($P < 0.0001$). Mice injected
with saline survived an average of 7.7 days, while rat
PEG-SCF¹⁻¹⁶⁴ treated mice survived an average of 9.4
days (Figure 45). The results presented in Figure 45
represent the compilation of 4 separate experiments with
35 30 mice in each treatment group.

The increased survival of mice treated with rat PEG-SCF¹⁻¹⁶⁴ suggests an effect of SCF on the bone marrow cells of the irradiated animals. Preliminary studies of the hematological parameters of these animals show slight increases in platelet levels compared to control animals at 5 days post irradiation, however at 7 days post irradiation the platelet levels are not significantly different to control animals. No differences in RBC or WBC levels or bone marrow cellularity have been detected.

B. Survival of Transplanted Mice Treated with SCF

Doses of 10% femur of normal Balb/c bone marrow cells transplanted into mice irradiated at 850 rad can rescue 90% or greater of animals (data not presented). Therefore a dose of irradiation of 850 rad was used with a transplant dose of 5% femur to study the effects of rat PEG-SCF¹⁻¹⁶⁴ on survival. At this cell dose it was expected that a large percentage of mice not receiving SCF would not survive; if rat PEG-SCF¹⁻¹⁶⁴ could stimulate the transplanted cells there might be an increase in survival. As shown in Figure 46, approximately 30% of control mice survived past 8 days post irradiation. Treatment with rat PEG-SCF¹⁻¹⁶⁴ resulted in a dramatic increase of survival with greater than 95% of these mice surviving out to at least 30 days (Figure 46). The results presented in Figure 46 represent the compilation of results from 4 separate experiments representing 20 mice in both the control and rat PEG-SCF¹⁻¹⁶⁴ treated mice. At higher doses of irradiation, treatment of mice with rat PEG-SCF¹⁻¹⁶⁴ in conjunction with marrow transplant also resulted in increased survival (Figure 47). Control mice irradiated at 950 rads and transplanted with 10% of a femur were dead by day 8, while approximately 40% of mice treated

with rat PEG-SCF¹⁻¹⁶⁴ survived 20 days or longer. 20% of control mice transplanted with 20% of a femur survived past 20 days while 80% of rSCF treated animals survived (Figure 47).

5

C. Radioprotective Effects of SCF on Lethally Irradiated Mice Without a Bone Marrow Transplant.

The effects of SCF administration prior to
10 irradiation were compared to the effects of SCF administration post-irradiation.

Female BDF1 mice (Charles River Laboratories, were used. All mice were between 7 and 8 weeks old and averaged 20-24 g each. Irradiation consisted of a
15 lethal split dose of 575 RADS each (total 1150 RADS) delivered 4 hours apart from a Gamma Cell to 40 dual cobalt source, (Atomic Energy Of Canada Limited).

In the experiment shown in Figure 19-1, the ability of SCF, administered prior to irradiation, to
20 save mice from an otherwise lethal exposure was tested. Rat SCF, purified from E. coli as in Example 10 and modified by the addition of polyethylene glycol as in Example 12, was administered to two groups of mice (n=30), either intra-peritoneally or intravenously at a
25 dose of 100 µg/kg. Control animals received excipient only which consisted of phosphate-buffered saline, 0.1% fetal bovine serum. The times of administration were t = -20 hours and t = -2 hours to the irradiation event (t=0). The survival of the animals was monitored
30 daily. The results are shown in Figure 48. Both routes of administration of rat SCF-PEG enhanced survival of the irradiated mice. At 30 days post irradiation, 100% of the animals treated with SCF were alive, whereas only 35% of the animals in the control group were alive.
35 Since similar experiments, outlined in Example 19 A where SCF was administered post-irradiation only,

yielded different results, the two modes of administration were compared directly in a single experiment. The experiment was performed as described above for Figure 49 except the groups were as follows (irradiation was at $t = 0$): group 1, control; group 2, rat SCF-PEG administered at $t = -20$ hours and $t = -2$ hours; group 3, rat SCF-PEG administered at $t = -20$ hours, $t = -2$ hours, and $t = +4$ hours; and group 4, rat SCF-PEG administered at $t = +4$ hours only. Both groups receiving rat SCF-PEG prior to irradiation survived at 95-100% at day 14 (groups 2 and 3). In accordance with the experiment described in Example 19 A, the animals receiving rat SCF-PEG post irradiation only did not survive the irradiation event, although they survived longer than controls.

These experiments demonstrate the utility of SCF administration to protect against the lethal effects of irradiation. These protective effects are most effective when SCF is administered prior to the irradiation event as well as after. This aspect of in vivo activity of SCF can be utilized in dose intensification regimes in anti-neoplastic radiotherapy.

EXAMPLE 20

Production of Monoclonal Antibodies Against SCF

8-week old female BALB/c mice (Charles River, Wilmington, MA) were injected subcutaneously with 20 μ g of human SCF¹⁻¹⁶⁴ expressed from E. coli in complete Freund's adjuvant (H37-Ra; Difco Laboratories, Detroit, MI). Booster immunizations of 50 μ g of the same antigen in Incomplete Freund's adjuvant were subsequently administered on days 14, 38 and 57. Three days after the last injection, 2 mice were sacrificed and their spleen cells fused with the sp 2/0 myeloma line according to the procedures described by Nowinski et al., [Virology 93, 111-116 (1979)].

The media used for cell culture of sp 2/0 and hybridoma was Dulbecco's Modified Eagle's Medium (DMEM), (Gibco, Chagrin Falls, Ohio) supplemented with 20% heat inactivated fetal bovine serum (Phibro Chem., Fort Lee, NJ), 110 mg/ml sodium pyruvate, 100 U/ml penicillin and 100 mcg/ml streptomycin (Gibco). After cell fusion hybrids were selected in HAT medium, the above medium containing 10^{-4} M hypoxanthine, 4×10^{-7} M aminopterin and 1.6×10^{-5} M thymidine, for two weeks, then cultured in media containing hypoxanthine and thymidine for two weeks.

Hybridomas were screened as follows:
Polystyrene wells (Costar, Cambridge, MA) were sensitized with 0.25 μ g of human SCF¹⁻¹⁶⁴ (E. coli) in 50 μ l of 50 mM bicarbonate buffer pH 9.2 for two hours at room temperature, then overnight at 4°C. Plates were then blocked with 5% BSA in PBS for 30 minutes at room temperature, then incubated with hybridoma culture supernatant for one hour at 37°C. The solution was decanted and the bound antibodies incubated with a 1:500 dilution of Goat-anti-mouse IgG conjugated with Horse Radish Peroxidase (Boehringer Mannheim Biochemicals, Indianapolis, IN) for one hour at 37°C. The plates were washed with wash solution (KPL, Gaithersburg, MD) then developed with mixture of H₂O₂ and ABTS (KPL). Colorimetry was conducted at 405 nm.

Hybridoma cell cultures secreting antibody specific for human SCF¹⁻¹⁶⁴ (E. coli) were tested by ELISA, same as hybridoma screening procedures, for crossreactivities to human SCF¹⁻¹⁶² (CHO). Hybridomas were subcloned by limiting dilution method. 55 wells of hybridoma supernatant tested strongly positive to human SCF¹⁻¹⁶⁴ (E. coli); 9 of them crossreacted to human SCF¹⁻¹⁶² (CHO).

Several hybridoma cells have been cloned as follows:

<u>Monoclonal</u>	<u>IgG Isotype</u>	<u>Reactivity to human SCF¹⁻¹⁶² (CHO)</u>
4G12-13	IgG1	No
6C9A	IgG1	No
8H7A	IgG1	Yes

5

Hybridomas 4G12-13 and 8H7A were deposited with the ATCC on September 26, 1990.

EXAMPLE 21

10 Synergistic Effect of SCF and Other Growth Factors.

A. Synergistic Effect of SCF and G-CSF in Rodents

15 Lewis rats, male, weighing approximately 225 gms, were injected intravenously via the dorsal vein of the penis with either polyethylenesporeglycol-modified ratSCF-PEG (Examples 10 and 12), recombinant human G-CSF, a combination of both growth factors, or with carrier consisting of 1% normal rat serum in
20 sterile saline. Quantitative peripheral blood and bone marrow differentials were performed at various timepoints as previously described [Hulse, Acta Haematol. 31:50 (1964); Chervenick et al., Am. J. Physiol. 215: 353 (1968)]. Histologic
25 examination of the spleen was performed with Bouin's-fixed paraffin-embedded sections stained with hematoxylin-and-eosin as well as by the Giemsa method. The numbers of normoblasts, megakaryocytes, and mast cells per 400X or 1000X high power field (HPF) in the
30 spleen was quantitated by counting the number of each cell type in randomly selected fields of the red pulp. Increases in circulating numbers of neutrophils over extended time periods were when so stated calculated by planimetry as previously described. [Ulich et al.,
35 Blood 75:48 (1990)]. Data is expressed as the mean plus-or-minus one standard deviation and statistical analysis is by the unpaired t-test.

A single coinjection of ratSCF-PEG (25 ug/rat) plus G-CSF (25 ug/rat) causes an increase in circulating neutrophils that is approximately additive (Figure 50 CSF) as compared to ratSCF-PEG alone (25 ug/rat) or G-CSF alone (25 ug/rat) as measured by planimetry over a 35 hour time period. The kinetics of ratSCF-PEG plus G-CSF-induced peripheral neutrophilia reflect the combined effect of the differing kinetics of ratSCF-induced neutrophilia peaking at 6 hours and G-CSF-induced neutrophilia peaking at 12 hours (Figure 50). The bone marrow at 6 hours after a single coinjection of ratSCF-PEG plus G-CSF (Table 18) shows a greater than additive decrease in mature marrow neutrophils ($9.94 \pm 0.3 \times 10^6$ PMN/humerus in carrier control rats vs. $2.11 \pm 0.3 \times 10^6$ PMN/humerus in ratSCF-PEG plus G-CSF-treated rats, 79% decrease) as compared to ratSCF-PEG alone-treated rats ($7.55 \pm 0.2 \times 10^6$ PMN/humerus, 24% decrease) or G-CSF alone-treated rats ($5.55 \pm 0.5 \times 10^6$ PMN/humerus, 44% decrease). A significant increase in myeloblasts and promyelocytes was seen in ratSCF-PEG, G-CSF-, and ratSCF-PEG plus G-CSF-treated rats at 6 hours as compared to carrier controls (Table 18), but no significant increase in any form of immature myeloid cells is noted in ratSCF-PEG plus G-CSF-treated rats as compared to ratSCF-PEG alone- or G-CSF alone-treated rats. A significant increase in myeloblasts is noted at 24 hours, however, in the ratSCF-PEG plus G-CSF group as compared to either ratSCF-PEG, G-CSF, or carrier alone ($p < 0.01$, Table 19).

Daily coinjection of ratSCF-PEG (25 ug/rat) plus G-CSF (25 ug/rat) for one week causes a highly synergistic increase in circulating neutrophils (Figure 51) as compared to ratSCF-PEG alone (25 ug/rat) or G-CSF alone (25 ug/rat). A marked linear increase rise in the number of circulating neutrophils occurs between day 4 and 6 after the coinjection of ratSCF-PEG

plus G-CSF to $41.4 \pm 1.2 \times 10^3$ PMN/mm³ at 24 hours after the last injection of the week as compared to $10.6 \pm 3.6 \times 10^3$ PMN/mm³ in G-CSF treated rats and $2.4 \pm 1.3 \times 10^3$ PMN/mm³ in ratSCF-PEG alone treated rats (Figure 51). A
5 more detailed kinetic study of ratSCF-PEG plus G-CSF-induced neutrophilia after the last injection of the week showed that the peak of circulating neutrophils occurs at 12 hours and reaches a level of $69.2 \pm 2.5 \times 10^3$ PMN/mm³ as compared to $25.3 \pm 0.3 \times 10^3$ PMN/mm³ in
10 G-CSF-treated rats and $5.6 \pm 3.4 \times 10^3$ in ratSCF-PEG-treated rats (Figure 52). The neutrophils of ratSCF-PEG plus G-CSF-treated rats were extremely hypersegmented (Figure 52). In addition to the overwhelming increase
in mature neutrophils in the circulation, an increase in
15 immature myeloid forms was noted as well as the appearance of immature monocytoid forms, rare macrophage-like cells that contained vacuoles and ingested erythroid or lymphoid cells, rare basophils, rare mononuclear promegakaryocytic forms and occasional
20 late normoblasts in peripheral blood smears. As many as 3% of the nucleated circulating blood cells were normoblasts in some of the peripheral blood smears of ratSCF-PEG plus G-CSF-treated rats after daily treatment for one week.

25 Two of the four rats in the ratSCF-PEG plus G-CSF-treated group died (one on the fifth day and one on the sixth day of the experiment), one of the surviving rats appeared ill on the day of sacrifice (the seventh day), and both of the surviving rats were
30 thrombocytopenic. None of the rats in the ratSCF-PEG alone, G-CSF alone, or carrier control groups showed any evidence of morbidity or were thrombocytopenic.

The bone marrow at 24 hours after the daily coinjection of ratSCF-PEG plus G-CSF for one week
35 demonstrated a synergistic increase in mature neutrophils from $10.6 \pm 0.6 \times 10^6$ PMN/humerus in carrier

controls, $14.5 \pm 1.0 \times 10^6$ PMN/humerus in ratSCF-PEG alone-treated rats, and $28.5 \pm 2.1 \times 10^6$ PMN/humerus in G-CSF alone-treated rats (Table 20). The neutrophils in the marrow are generally hypersegmented and are often hypergranulated due to an increase in primary azurophilic granules.

The spleens of ratSCF-PEG plus G-CSF-treated rats were much larger and histologic examination showed increased myelopoiesis, erythropoiesis, and megakaryocytopoiesis as compared to the spleens of control or single factor-treated rats. The spleens of ratSCF-PEG plus G-CSF-treated rats showed atrophy of the white pulp concomitant with a tremendous expansion of the red pulp which was replaced by nearly confluent extramedullary hematopoiesis. The number of granulocytic precursors (myeloblasts to metamyelocytes) was readily seen by scanning histologic sections of the spleen to be markedly increased in the ratSCF-PEG plus G-CSF group as compared to all other groups. Interestingly, the number of normoblasts in the spleen was also increased in the ratSCF-PEG plus G-CSF group (4.1 ± 5.8 in the ratSCF-PEG alone group, 0 ± 0 in the G-CSF alone group, and 36.4 ± 26.1 in the ratSCF-PEG plus G-CSF group; $18 \times 1,000$ HPF/spleen/rat; $p < 0.0001$ comparing ratSCF-PEG plus G-CSF vs. ratSCF-PEG alone). The number of megakaryocytes in the spleen was also significantly increased in the ratSCF-PEG plus G-CSF group (1.8 ± 1.5 in the ratSCF-PEG alone group, 2.0 ± 1.1 in the G-CSF alone group, and 5.2 ± 3.1 in the ratSCF-PEG plus G-CSF group; 12×400 HPF/spleen/rat; $p < 0.0001$ comparing ratSCF-PEG plus G-CSF to either ratSCF-PEG or G-CSF alone).

These results demonstrate that the in vivo combination of ratSCF-PEG and G-CSF causes a synergistic myeloid hyperplasia in the bone marrow and spleen and a synergistic increase in circulating neutrophils. The synergism between a single dose of ratSCF-PEG and G-CSF

becomes most dramatically apparent as a rapidly increasing number of circulating neutrophils between 4 and 6 hours after commencement of administration of growth factors. Daily coinjection plus G-CSF for one week causes a highly synergistic increase in circulating neutrophils as compared to ratSCF-PEG alone or G-CSF alone.

B. Synergistic Effect of SCF and Other Growth Factors in Canines.

10

Though single factors such as G-CSF have been shown to have important effects on hematopoietic recovery, the combination of SCF with G-CSF has a dramatic hematologic response. In the first set of experiments, 3 normal dogs were treated with recombinant canine SCF alone at 200 µg/kg/day subcutaneously or by continuous intravenous infusion. These animals responded with an increase in the white blood cell count to 30-50,000/mm³, from a baseline of 10-15,000/mm³ by day 8-12. When another group of normal dogs were treated for 28 days with recombinant canine SCF (200 µg/kg/day SCF and G-CSF (10 µg/kg/day SC), the white blood cell count increased from a normal range of 10-11,000/mm³ to 200-240,000 cells /mm³ by day 17-21. This demonstrates that the effects of SCF are dramatically enhanced in combination with other hematopoietic growth factors. Similarly, in vitro data show that SCF in combination with EPO dramatically enhances BFU-E growth (number and size, see Example 9), again demonstrating that combinations of hematopoietic growth factors are more effective in eliciting a hematopoietic response and/or may allow for lower doses of other factors to elicit the same response.

35

EXAMPLE 22

The Use of SCF in Hematopoietic Transplantation

5 A. The Effects of SCF on Amplification of Bone Marrow and Peripheral Blood Hematopoietic Progenitors

The effects of SCF administration on circulating hematopoietic progenitors in normal baboons was studied.

10 The experimental design was identical to that described in Example 8C. Briefly, normal baboons were administered 200 µg/kg/day human SCF¹⁻¹⁶⁴, produced in E. coli as in Example 10 and modified by the addition of polyethylene glycol as in Example 12, as a continuous intravenous

15 infusion. At various times bone marrow and peripheral blood was harvested and cultured at a density of 2×10^5 per ml in Iscoves' Modified Dulbecco's Medium (Gibco, Grand Island, NY) in 0.3% (W/v) agar (FMC, Rockland, ME), supplemented with 25% fetal bovine serum (Hyclone,

20 Logan, UT), and 10^{-4} 2-mercaptoethanol in 35 mm culture dishes (Nunc, Naperville, IL). Cells were cultured in the presence of human IL-3, IL-6, G-CSF, GM-CSF, SCF at 100 ng/ml and EPO at 10 U/ml. Cultures were incubated at 37 °C in 5% CO₂ in a humidified incubator. At day 14 of

25 culture, colonies were enumerated using an inverted microscope. Macroscopic BFU-E were defined as those greater than 0.5 mm in diameter.

Marrow CFU-GM and BFU-E were assayed from four baboons before and at the end of the SCF infusion. The

30 number of colonies per 10^5 cells, i.e., CFU-GM (41+/-12 pre-SCF, 36+/-post-SCF) and BFU-E (78+/-28 pre-SCF, 52+/-26 post-SCF), were not statistically different. Given the dramatic increases in marrow cellularity, the absolute numbers of CFU-GM and BFU-E were estimated to

35 be increased.

A fifth baboon given SCF was studied weekly for changes in peripheral blood and marrow colony-forming cells. In marrow, the incidence of CFU-GM increased 1.1 to 1.3 fold and BFU-E increased 2.5 to 6.5 fold. In peripheral blood, however, the incidence of colony-forming cells was markedly increased (25 to 100 fold), and absolute numbers of colony-forming cells were increased up to 96 fold for CFU-GM, 934 fold for BFU-E, and greater than 1000 fold for the most primitive colony-forming cells, CFU-MIX. This expansion of colony-forming cells was apparent after as little as seven days of SCF administration and was maintained throughout the period that SCF was given.

15 B. Use of SCF in Bone Marrow Transplantation

As noted above, there are several ways that SCF is useful to improve hematopoietic transplantation. One method, as illustrated above is to use SCF to augment the harvest of bone marrow and/or peripheral blood progenitors and stem cells by pretreating the donor with SCF. Another use is to treat the recipient of the transplanted cells with SCF after the patient has been infused. The recipient is treated with SCF alone or in combination with other early and late acting recombinant hematopoietic growth factors, including EPO, G-CSF, GM-CSF, M-CSF, IL-1, IL-3, IL-6, etc.

SCF alone enhances hematopoietic recovery following bone marrow transplantation. A variety of experimental variables have been tested in a canine model of bone marrow transplantation, Schuening et al., 76 636-640. In one set of experiments for the present invention, dogs received either G-CSF or SCF after 920 cGy of total body irradiation and 4×10^8 mononuclear marrow cells per kilogram from a DLA-identical

littermate. The hematologic recovery, as measured by day of neutrophil recovery to 500 or 1000/mm³, is accelerated when either SCF or G-CSF is administered compared to control animals that received no growth factor (Table 21). Recovery was 2-6 days earlier in animals that received SCF than it was in those that received no growth factor. As noted above, combinations of appropriate growth factors with SCF will accelerate and enhance the response to those growth factors following hematopoietic transplantation.

TABLE 21
Effects of rcG-CSF and SCF on Recovery From
DLA-identical Littermate Marrow Transplantation¹

Treatment	Recovery of ANC > 500 mm ³	Recovery of ANC > 1000/mm ³
Control	Day 10	Day 14
rcG-CSF ²	Day 7	Day 8
rcSCF ³ #1	Day 7	Day 8
rcSCF ³ #2	Day 8	Day 9

¹920 cGY TBI followed by infusion of 4 x 10⁸ mononuclear cells per kg DLA-identical littermate bone marrow

²rcG-CSF administered 10 µg/kg/day_{sc} for 10 days following transplant

³rcSCF administered 200 µg/kg/day_{sc} for 10 days following transplant

- 2 -

This aspect of *in vivo* biological activity can be utilized to enhance the recovery from marrow ablative therapy if the peripheral blood or bone marrow is harvested after SCF administration and then re-

5 infused after the ablative regimen (i.e., in bone marrow transplantation or peripheral blood autologous transplantation).

EXAMPLE 23

10 Effect of SCF on Platelet Formation

Balb/c mice (female, 6-12 weeks of age, Charles River) were treated with rratSCF-PEG (100 ug/kg/day) or excipient control, subcutaneously, 1 time

15 daily for 7 days (n=7). Blood was sampled through a small incision in the lateral tail vein on the indicated days after cessation of SCF treatment. Twenty microliters blood were collected directly into 20 ul microcapillary tubes and immediately dispensed into the

20 manufacturers diluent for the Sysmex Cell Analyzer. Data points are the mean of the data, error bars are standard error of the mean. Blood platelet counts were determined at the time points indicated in Figure 53. Platelet counts rose to approximately 160% of control

25 values by Day 4 post-SCF, fell to normal by Day 10, and rose again to 160% of normal by Day 15. Platelet counts stabilized at control values by Day 20.

A dose response curve of the SCF effect on platelet counts was generated when Balb/c mice were

30 treated as above with 10, 50, or 100 ug/kg/day rratSCF-PEG (n=7). Blood was collected and analyzed on the fourth day following cessation of SCF treatment. These data are shown in Figure 54 and demonstrate that concentrations of rratSCF-PEG between 50-100 ug/kg/day

35 are optimal in inducing a rise in platelet counts. Recombinant rat SCF-PEG administration to normal mice

also resulted in an increase in platelet size and in the number of megakaryocytes found in the spleen and bone marrow (Table 22). Rodent megakaryocytes were identified by expression of the enzyme

- 5 acetylcholinesterase (ACH+) which was detected by cytochemical assays, [Long, Blood 58:1032 (1981)].

Certain similarities were noted between mice given SCF and mice during rebound thrombocytosis after experimental induction of thrombocytopenia. Figure 55
10 demonstrates one model of experimental thrombocytopenia, namely that of treatment of 5-fluorouracil (5-FU). Balb/c mice were either untreated or treated intravenously with 5-fluorouracil (150 mg/kg) on Day 0
(n=5). Blood analyses were performed on the indicated
15 days as in legend to Figure 53. Error bars are present, but not discernable, in some of the control points. As has been demonstrated in the past [Radley et al., Blood 55:164 (1980)], animals become thrombocytopenic by Day 5 post-5-FU. However, by Day 12 animals were in a
20 state of rebound thrombocytosis where platelet counts far exceed normal (the "overshoot" effect). After Day 12, platelet counts appeared to cycle from normal to high levels throughout the 40 day testing period. As shown in Figure 56, megakaryocyte numbers also rise dramatically
25 after 5-FU appearing first in the bone marrow (Panel A) and then in the spleen (Panel B). The megakaryocyte numbers were determined in parallel with that shown in Figure 55. Two Balb/c mice per group were sacrificed at the indicated days. Cells from bone marrow (Panel A) or
30 spleen (Panel B) were aliquoted at 100,000/well of a microtiter plate and stained for acetylcholinesterase according to published procedures, Long et al., Immature megakaryocytes in the mouse: Morphology and quantitation by acetlycholinesterase staining. Blood 58: 1032,
35 1981. Data points are the percentage of ACH+ cells per well for individual animals.

Platelet volumes also increase after 5-FU (Figure 57). The data in this figure were generated from the same blood samples collected in Figure 55. Mean Platelet Volume (MPV) is one of the parameters analyzed by the Sysmex Cell Analyzer.

The possibility of a relationship between SCF and the physiological regulator of platelet production induced in the 5-FU thrombocytopenic model was explored. 5-FU was given to normal mice and SCF mRNA expression levels quantitated in bone marrow cells collected on the days indicated in Figure 58. In Figure 58, one million cells were lysed in SDS buffer and the lysate was analyzed for the presence of mRNA specific for murine SCF. Probes for mouse SCF or human actin mRNA (which detects the corresponding murine mRNA) were generated by runoff transcription of cloned gene regions in vectors containing SP6 or T7 promoters using ³⁵S-UTP according to standard protocols (Promega Biotech), or from synthetic oligonucleotide partial duplexes, Mulligan et al., Nuc. Acids Res. 15:8783 (1987). RNA sense strand standards for quantitation of the hybridization assays were produced by runoff transcription of the same region in the direction opposite to the direction of probe synthesis using tracer quantities of ³⁵S-UTP and 0.2 mM unlabeled UTP.

SCF or actin mRNA levels were quantitated as follows. Bone marrow cells were explanted from animals at the given time post-5FU, enriched for light density cells by centrifugation on 65% Percoll (Pharmacia; Piscataway, NJ) and lysed at 3 x 10⁶ nucleated cells/ml in 0.2% SDS, 10 mM Tris pH 8, 1 mM EDTA, 20 mM dithiothreitol and 100 ug/ml proteinase K (Boehringer Mannheim; Indianapolis, IN). Samples (30 ul) were added to 70 ul of hybridization mix consisting of 30 ug/ml yeast tRNA, 30 ug/ml carrier DNA, 145,000 CPM/ml ³⁵S-labeled probe in 3.0-3.7 M sodium phosphate, pH 7.2

(depending on length of probe). Samples were incubated at 84°C for 2-3 hours then cooled to room temperature before addition of RNase A to .03 mg/ml and RNase T1 to 5000 U/ml. Samples were incubated at 37°C for

5 20 minutes before addition of 120 ul of .0025% bromophenol blue in formamide. Entire sample was then loaded onto 3.8 ml Sephacryl S200 Superfine gel filtration column (0.7 cm x 10 cm) and eluted with 2.0 mls of 10 mM Tris pH 8, 1 mM EDTA, 50 mM NaCl.

10 Effluents containing hybridized RNA duplexes were collected directly into scintillation vials. After addition of 5 mls Liquiscint (New England Nuclear; Boston, MA) samples were counted 20 minutes or to 3% error. CPM were converted to molecules mRNA by

15 comparison to the linear portion of the standard curve (correlation coefficient = 0.97). The data point for each sample is the mean of replicate tests; bone marrow samples from 3 individual animals were taken for each time point so that the data shown is the mean of those

20 determinations. Error bars are standard error of the mean. Statistical significance is assigned as described above.

SCF mRNA levels rose dramatically at Days 5 and 7, coinciding exactly with the nadir of platelet

25 counts immediately preceding thrombocytosis (Figure 58).

The data in this section show that SCF is active as a thrombopoietic agent in vivo and furthermore that SCF may be involved in the physiological regulation of platelet production after 5-FU-induced thrombocytopenia.

30

35

Table 22. Megakaryocyte and platelet parameters measured on fourth day following SCF administration in vivo.

Factor	Platelet		%Ach+ Cells in	
	Count	MPV*	Spleen	Marrow
none	1018 +/- 29	6.07 +/- 0.5	.22 +/- .3	.02 +/- .01
SCF**	1429 +/- 56	6.24 +/- .05	.85 +/- .9	.59 +/- .05

*MPV; mean platelet volume

**ratSCF-PEG administered SC 2 x daily for 7 days at 100 ug/kg/day. Data were collected 4 days later after last injection.

EXAMPLE 24

Treatment of Bone Marrow Failure States

A variety of congenital and acquired disorders of hematopoiesis have been reported to cause clinically significant reductions in the number of mature circulating peripheral blood cells of one or more lineages. Therefore, the existing data supports that these disorders are treatable with SCF. For example, aplastic anemia is a clinical syndrome characterized by pancytopenia due to reduced or absent production of blood cells in the bone marrow. It is heterogeneous in severity, etiology and pathogenesis.

Most attention has focused on abnormalities of the hematopoietic stem cell, microenvironment or immunologic injury of one of these. The response to immunosuppressive therapy is variable and incomplete. Because aplastic anemia is a defect of the hematopoietic stem

cell or proliferative signals from the microenvironment, and is modeled by the Steel mouse [Zsebo et al., Cell 63 213 (1990)], this disorder is successfully treated with SCF.

5 Another bone marrow failure disorder which is responsive to SCF is Diamond-Blackfan anemia (DBA) or congenital pure red cell aplasia. This congenital abnormality results in a selective defect in the production of red blood cells and often results in
10 chronic transfusion dependency. In vitro data indicate that the defect is overcome by the addition of exogenous SCF. Bone marrow from patients with DBA (or control marrow) was cultured with or without SCF (100 ng/ml) in the presence of erythropoietin (EPO) (1-5 U/ml), EPO
15 plus IL-3 (1-1000 U/ml), EPO plus GM-CSF (>100 U/ml), or EPO plus lymphocyte-conditioned media (2-5%). Culture of bone marrow from patients with DBA demonstrate two patterns of response to SCF. The majority were hyper-responsive to SCF and showed approximately 3 fold
20 increase in the frequency of BFU-E at less than or equal to 10 ng/ml, as well as an increase in the size of BFU-E at concentrations up to 200 ng/ml. Control marrow demonstrated only a 1.5 fold increase in frequency of BFU-E. This pattern of response to SCF could indicate a
25 defect in endogenous SCF and/or its production by the microenvironment in this group of patients with DBA. The other group of patients with DBA demonstrated an increase in the frequency of BFU-E at concentrations of SCF greater than or equal to 50 ng/ml. This pattern of
30 response reflects an intrinsic defect in the receptor for SCF (c-kit) on the progenitor cell. In either case (abnormal production of SCF by the microenvironment or decreased stimulation of the hematopoietic progenitor by SCF) SCF overcomes the block to hematopoiesis which
35 characterizes bone marrow failure syndromes such as DBA.

Other bone marrow failure syndromes that are treatable with SCF include, but are not limited to: Fanconi's anemia, dyskeratosis congenita, amegakaryocytic thrombocytopenia, thrombocytopenia with absent radii, and congenital agranulocytosis (e.g. Kostmann's syndrome, Shwachman-Diamond syndrome) as well as other causes of severe neutropenia such as idiopathic and cyclic neutropenia. Severe chronic neutropenia congenital, cyclic or idiopathic are treatable with recombinant G-CSF.

Cyclic neutropenia, in particular, is a defect in the regulation of stem cell division since other lineages (e.g., platelet, erythrocyte and monocyte) are also effected. In the canine model of cyclic neutropenia, the cycling of neutrophils, as well as other lineages, is sharply reduced or even eliminated by SCF treatment. A typical dog with cyclic neutropenia was treated with canine SCF (recombinant canine SCF) at 100 mg/kg/day subcutaneously over several weeks. The typical 21 day cycle for neutrophils was eliminated during the first predicted cycle and the second predicted nadir was significantly attenuated. This is in contrast to treatment with G-CSF which increases the frequency and amplitude of neutrophil cycling, but does not eliminate it. Thus, SCF is useful in treating a variety of bone marrow failure syndromes, either alone or in combination with other hematopoietic growth factors.

EXAMPLE 25

SCF Treatment of Patients With HIV-1 Infection

A. Source and Preparation of Peripheral Blood Mononuclear Cells

Leukopaks were obtained from HIV-, CMV-, and EBV-seronegative normal donors from the American Red

Cross. Peripheral blood was obtained from 6 patients with HIV-infection after informed consent was obtained. Two patients were asymptomatic, one had AIDS-related complex and three had AIDS. None of the 6 patients had received zidovudine within the last six months. None of the patients were anemic (hemoglobin < 135 g/L) at the time of study. All studies were conducted in accordance with UCLA Human Subject Protection Committee regulations.

Peripheral blood mononuclear cells were isolated from leukopaks and peripheral blood using ficoll-hypaque sedimentation followed by extensive washing with Hank's Balance Salt Solution (HBSS). Blood cells were enumerated and viability ascertained by trypan blue dye exclusion.

B. Burst Forming Unit Erythro (BFU-E) Assay

Assays for BFU-E were performed in a standard protocol using normal human bone marrow as the control. Heparinized blood was diluted with an equal volume of HBSS (GIBCO, Grand Island, NY), layered over Ficol-Paque (Pharmacia, Piscataway, NJ) and centrifuged at 400 g for 30 minutes at room temperature. Light density cells (s.g. <1.077) were collected and washed twice in HBSS. Cells were resuspended in Iscove's Medium with 10% Fetal Bovine Serum (GIBCO, Grand Island, NY) at a concentration of 1×10^7 /ml. Cells (1×10^5) were cultured in Iscove's Media supplemented with 5×10^{-5} M 2-Mercaptoethanol (2ME) (Sigma Chemicals, St. Louis, MO), 30% Fetal Bovine Serum (GIBCO, Grand Island, NY), and either 1 or 4 units of human recombinant erythropoietin (Amgen Inc., Thousand Oaks, CA) in 0.3% agar. Four concentrations of *E. coli* derived human stem cell factor (hSCF¹⁻¹⁶⁴), obtained as described in Examples 6 and 10, were added (0,10,100 and

1000 ng/ml). Zidovudine (AZT) was added to the mixture resulting in final concentrations of 0, 0.01 μ M, 0.1 μ M, 1.0 μ M. Erythroid burst colonies were scored after 14 days of culture in a humidified atmosphere containing 5% CO₂. Each assay was done in duplicate and colonies with >50 cells present on day 14 with hemoglobinization were scored as BFU-E.

The 50% inhibitory concentration for zidovudine was calculated by expressing the mean of four determinations of BFU-E for each level of zidovudine and huSCF as a percentage of control (no added zidovudine). Linear regression was used to calculate the slope of inhibition. The 50% inhibitory concentration was calculated by interpolation and the value used as the exponent for the base of 10. This results in direct calculation of the ID₅₀. The r² for all the slopes were >0.90.

20 C. Effects of HuSCF on Stimulated Peripheral Blood Mononuclear Cells

Peripheral blood mononuclear cells were isolated from the leukopaks of two additional normal donors as described above. Cells were resuspended in Iscove's Modified Dulbecco's Medium containing 20% fetal bovine serum, penn/strep, 1.0% PHA (Sigma Chemical, St. Louis, Mo.) and 10 units/ml of interleukin-2 (Amgen Inc. Thousand Oaks, CA). Four concentrations of human stem cell factor (0, 10, 100, 1,000 ng/ml) were added to the media. Complete lymphocyte subset analysis of cellular antigens were analyzed in duplicate by two color fluorescent cytometry on day 0, 3, 7 and 10. Differences in percentages of cell populations were detected using independent and paired t-tests (2-tailed). Comparisons were made between drug-treated and non-drug-treated values for a single day and between

single days values and baseline. Cytometric analysis was done in duplicate.

D. Results

5

Exposure of peripheral blood mononuclear cells to erythropoietin and human stem cell factor (HuSCF) resulted in a dose-dependent increase in BFU-E formation in the 2 normal patients studied (Figure 59A).

- 10 Significant increases (up to 100%) were seen with concentrations of human stem cell factor between 10 and 1,000 ng/ml. Near maximal activity was seen at 10 ng/ml suggesting that lower concentrations may be active. There were significant increases in BFU-E when the dose
15 of erythropoietin was increased from 1 IU to 4 IU/ml (Figure 59B). The colonies observed were significantly larger in size than the bursts seen in the absence of HuSCF.

- In the 6 HIV-infected individuals studied,
20 significant dose-dependent increases in BFU-E were also seen with HuSCF treatment (Figure 60). Although the number of BFU-E in the absence of HuSCF was markedly reduced compared to normal (range 2-26 BFU-E/ 10^5 peripheral blood mononuclear cells compared to
25 approximately 74 BFU-E/ 10^5 PBMC for normals), the percentage increases in BFU-E were significantly higher in the HIV-infected individuals. Near normal numbers of BFU-E were obtained for 2 individuals at the 1,000 ng/ml concentration of HuSCF. Although the absolute number of
30 BFU-E seen for some of the patients were still well below normal, all 6 individuals responded in vitro to HuSCF.

- Because previous studies showed that cytokines could alter the intracellular uptake or intracellular
35 metabolism of deoxynucleosides. [Perno et al., J. Exp. Med. 169:933(1989)] the capacity of hSCF to modulate the

inhibition of red cell progenitors by zidovudine was evaluated. Each of the normals and all of the HIV individuals had BFU-E assays performed in the presence and absence of 3 concentrations of zidovudine and 4 concentrations of huSCF. As observed, (Figures 59 and size of BFU-E bursts) the addition of HuSCF markedly reduced inhibition of early red cell progenitors by zidovudine. Significant alterations in the 50% inhibitory dose of zidovudine for BFU-E was seen at all three concentrations of human stem cell factor. The IC₅₀ (fifty percent inhibitory concentration) ranged from 2.65 to 1376 μ M of zidovudine (Figure 61). All three of these inhibitory concentrations of zidovudine are well above normal serum levels obtained after 1,000 mg/day of zidovudine [Klecher et al., Clin. Pharmacol. Ther.; 41:407-12 (1987)]. Similar results were observed for all 6 individuals infected with HIV. However, because of the few number of red cell progenitors in 2 of the patients, the increases in the 50% inhibitory concentrations of zidovudine for BFU-E did not reach statistical significance. Nonetheless, the trends were clearly present and replicated the effects of human stem cell factor on BFU-E in the presence of zidovudine in the normal individuals.

The effect of SCF on the protection of bone marrow derived cells as well as peripheral blood progenitors (above) was examined. Normal human bone marrow was prepared as described above for peripheral blood progenitors. Bone marrow cells were exposed to different concentrations of AZT (zidovudine), and the protective effects of SCF for both erythroid as well as myeloid cells was determined in semi-solid cultures. Colonies were scored after 14 day incubation as described above. The results for the protection of bone marrow derived erythroid cells (Figure 62) and myeloid cells (Figure 63) are indicated. As is seen for

peripheral blood, SCF protects bone marrow cells from AZT as well. Another toxic compound used to fight the opportunistic infections associated with HIV infection is ganciclovir. Once again, SCF protects bone marrow cells against the toxic effects of ganciclovir for both erythroid development (Figure 64) and myeloid development (Figure 65).

In summary, this example details the effects of HuSCF on early red blood cell progenitors. Exposure to HuSCF in vitro resulted in a dose and time-dependent increase in red blood cell progenitors and significantly altered the inhibition of red cell progenitors by zidovudine. This was observed in both normal and HIV-infected study populations. HuSCF had no effect on HIV virus replication in primary monocytes or primary human lymphocytes nor did it alter the efficacy of 2',3',-dideoxynucleoside analogues. This is a significant difference from other cytokines which have effects on red cell progenitors such as granulocyte-macrophage colony-stimulating factor (GM-CSF) and interleukin-3 (IL-3). As shown in other studies [Koyanagi et al., Science 241:1773 (1981); Folks et al., Science 238:800 (1987); Hammer et al., Proc. Natl. Acad. Sci. USA 83:8734 (1986)], both GM-CSF and IL-3 significantly increase replication of HIV in partially purified primary peripheral blood monocytes.

These studies demonstrate that human stem cell factor (HuSCF) is an ideal candidate drug for use as adjunctive therapy in the treatment of HIV-related pancytopenia. This cytokine appears to directly stimulate human hematopoietic progenitor cells and synergizes with IL-7, G-CSF, GM-CSF, and IL-3 in the production of pre-B lymphocytes, megakaryocytes, monocytes, granulocytes, and mast cells [Martin et al., Cell 63:203-211 (1990); Zsebo et al., Cell, 63:213-224 (1990)].

EXAMPLE 26

Use of Stem Cell Factor to Facilitate Gene
Transfer into Hematopoietic Stem Cells

5 The in vitro survival and proliferation of
primitive stem cells is critical to the success of gene
transfer mediated by retroviral insertion or other known
methods of gene transfer. The effect of SCF on the in
vitro maintenance and/or proliferation of primitive
10 progenitor cells has been studied in two systems which
have been described previously [Bodine et al., Proc.
Natl. Acad. Sci. 86 8897-8901, 1989]. The first is a
pre-CFU-S assay wherein bone marrow cells are incubated
for up to six days in suspension culture in the presence
15 of growth factors. Aliquots are injected into lethally
irradiated mice and the mice sacrificed at 12-14 days for
quantitation of spleen focus formation. IL-3 and IL-6
synergize in enhancing the proliferation of CFU-S
between 2-6 days in culture. The second is a
20 competitive repopulation assay which measures the
effects of growth factors on recovery and biological
activity of cells capable of sustaining long-term
hematopoiesis. Cells from two congenic strains of mice
differing for a hemoglobin marker are incubated in
25 suspension independently, cells from one strain as a
control and cells from a second under experimental
conditions. After incubation, equal numbers of bone
marrow cells from both cultures are mixed and injected
into W/W^V recipients.
30 Rat SCF has been evaluated both in the pre-
CFU-S and competitive repopulation assays. SCF alone
has very little activity in the pre-CFU-S assay, similar
to IL-3 alone. For enhancing CFU-S activity, the
combination of SCF and IL-3 is equivalent to the
35 previous optimal combination of IL-3 and IL-6 whereas
the combination of SCF and IL-6 is 5-fold more active

than IL-3 and IL-6 (Figure 66). A most advantageous combination is SCF, IL-3 and IL-6; it is 6-fold more active than the combination of IL-3 and IL-6.

In the competitive repopulation assay, the
5 repopulating ability of cells cultured in the
combination of SCF and IL-6 is superior at 35 days
(short-term reconstitution) (Figure 67). A most
advantageous combination for long term reconstitution is
SCF, IL-3 and IL-6, approximately 1.5-fold greater than
10 any combination of two factors. Based on these data, a
most advantageous combination of soluble growth factors
for enhancing retroviral mediated gene transfer into
stem cells would be SCF, IL-3 and IL-6.

SCF presentation by stromal cells induces the
15 proliferation of primitive bone marrow progenitors. The
ultimate in vitro stimulus for proliferation of stem
cells is provided by stromal cell lines transfected with
human SCF cDNAs with sequences as shown in Figures 42
and 44. When human bone marrow is cultured on
20 artificial feeder layers expressing the membrane bound
form of human SCF 220 (Figure 44), there is a continued
proliferation of hematopoietic progenitors over time.
An example of this is given in Table 23. Stromal cells
derived from S1/S1 embryos prior to their death in utero
25 [Zsebo et al., Cell 63 213 (1990)] were transfected with
human SCF cDNAs (either expressing the 220, Figure 44 or
248, Figure 42, amino acid forms of SCF) and used as
feeder layers for human marrow. Briefly, adherent
layers were treated with mitomycin C and plated at
30 confluence in 6 well plates. Normal human bone marrow,
 7.5×10^5 adherence depleted cells, were plated in 5 ml
of Iscove's Modified Dulbeccos Medium (Gibco), 10% fetal
calf serum, and 10^{-6} M hydrocortisone onto the
transfected adherent layers. At the indicated time
35 points, cells were withdrawn and plated in semi-solid
agar using EPO and IL-3 as a stimulus. For the

experiment in Table 24, normal adherence depleted human bone marrow was first enriched for hematopoietic progenitors expressing the CD34 antigen using magnetic particle concentration [Dynal, Inc., Great Neck, NY] prior to plating on the adherent feeder cells. In this case, 3.5×10^4 cells were cultured on top of the adherent layers as described above. At the indicated time points, cells were withdrawn from the cultures and plated in semi-solid agar as described above. For both experiments, colony formation was enumerated after 14 days of culture in a humidified atmosphere. The generation of colony forming cells over time was enumerated. As is indicated, the membrane bound form of SCF (220 amino acid, Figure 44) is more potent at supporting hematopoiesis over time.

The Sl/Sl cell line expressing human SCF¹⁻²²⁰ amino acid form is advantageous for retroviral mediated gene transfer into hematopoietic stem cells. Human bone marrow is infected with retrovirus in the presence of mammalian cells expressing human SCF¹⁻²²⁰. In addition, the viral producer line optimally is transfected with the human SCF¹⁻²²⁰ gene and used for the viral infection as a co-culture.

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Table 23. Generation of colony forming cells from normal human bone marrow by cells expressing different splice variants of human SCF.

	Cells;	Days of Culture	CFU-Macs	CFU-GM	BFU-E	CFU-Mix
5	S1/S1-4	7	1.3+/-1	6+/-3	3+/-3	0
		14	0	0	0	0
		21	0	0	0	0
	S1/S1-4 SCF 220	7	31+/-13	51+/-8	3+/-2	0
		14	57+/-2	69+/-5	0	0
		21	46+/-16	23+/-13	0	0
10	S1/S1-4 SCF 248	7	57+/-14	89+/-7	11+/-8	1+/-1
		14	5+/-4	9+/-5	5+/-3	0
		21	1+/-1	0	0	0

Table 24. Generation of colony forming cells from CD34+ bone marrow cells expressing different splice variants of human SCF.

	Cells;	Days of Culture	CFU-Macs	Total colonies/culture well		
				CFU-GM	BFU-E	CFU-Mix
20	S1/S1-4	7	4+/-2	10+/-6	11+/-3	1+/-1
		14	0	0	0	0
		21	0	0	0	0
	S1/S1-4 SCF 220	7	90+/-7	70+/-2	18+/-10	13+/-4
		14	14+/-13	60+/-11	2+/-1	0
		21	36+/-3	23+/-5	0	0
25	S1/S1-4 SCF 248	7	260+/-64	135+/-20	80+/-20	15+/-5
		14	0	0	0	0
			0	0	0	

30

EXAMPLE 27

Further Characterization of Recombinant Human SCF Obtained from E. coli or CHO Cells

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As noted in Example 10, human [Met⁻¹]SCF¹⁻¹⁶⁴ from E. coli has amino acid composition and amino sequence expected from analysis of the

gene. Using the methods outlined in Example 2, it has been determined that human SCF¹⁻¹⁶⁵ obtained from E. coli as described in Example 10 also has the amino acid composition and amino acid sequence expected from analysis of the gene, and also retains Met at position (-1).

Purified E. coli-derived human [Met⁻¹]SCF¹⁻¹⁶⁴ and CHO cell-derived human [Met⁻¹]SCF¹⁻¹⁶² have been studied by methods indicative of secondary and tertiary structure. Fluorescence emission spectra, with excitation at 280 nm, have been obtained. These are shown in Figure 68. The molecules were dissolved in phosphate-buffered saline. The spectra consist of a single peak with a maximum at 325 nm, and a full width at half maximum (FWHM) of between 45 and 50 nm. Both the emission wavelength and the FWHM suggest that the single Trp is present in a hydrophobic environment, and that this environment is the same in both molecules.

Circular dichroism studies have also been carried out. Figure 69 shows the far ultraviolet (UV) spectra and near UV spectra (B) for the E. coli-derived SCF (solid lines) and CHO cell-derived SCF (dotted lines). The molecules were dissolved in phosphate-buffered saline. The far UV spectra contain minima at 208 nm and 222 nm. Using the Greenfield-Fasman equation [Greenfield and Fasman, Biochemistry 8, 4108-4116 (1969)], the spectra suggest 47% α -helix, while the method of Chang et al. [Anal. Biochem. 91, 13-31 (1978)] indicates about 38% α -helix, 33% β -sheet, and 29% disordered structure. The near UV spectra have minima at 295 nm and 286 nm attributable to tryptophan, minima at 261 nm and 268 nm attributable to phenylalanine, and minima at 278 probably attributable to tyrosine, with some overlap between chromophores. The results indicate that the aromatic chromophores are located in asymmetric

environments. Both the far UV and near UV results are the same for E. coli-derived SCF and CHO cell-derived SCF, indicating similarity of structure.

Second derivative infrared spectra in the amide I region ($1700-1620\text{ cm}^{-1}$) of the E. coli-derived SCF (A) and CHO cell-derived SCF (B) are shown in Figure 70. These spectra are related to polypeptide backbone conformation [Byler and Susi, Biopolymers 25, 469-487 (1986); Surewicz and Mantsch, Biochim. Biophys. Acta 952, 115-130 (1988)] and are essentially identical for the two proteins. Band assignments [Byler and Susi (1986), supra; Surewicz and Mantsch (1988), supra] allow one to estimate that the two SCFs have predominantly helical structures, ~31% α -helix and 19% 3_{10} -helix, with lesser fractions of β -strands (~25%), turns (~15%), and disordered structures (~14%).

Disulfide structure of various molecules referred to in previous examples have been determined. These include BRL 3A cell-derived natural rat SCF, E. coli-derived rat [Met⁻¹]SCF¹⁻¹⁶⁴, CHO cell-derived rat SCF¹⁻¹⁶², E. coli-derived human [Met⁻¹]SCF¹⁻¹⁶⁴, E. coli-derived human [Met⁻¹]SCF¹⁻¹⁶⁵, and CHO cell-derived human SCF¹⁻¹⁶². The methods used include those outlined in Example 2 for amino acid sequence and structure determination. The proteins are digested with proteases, and the resulting peptides isolated by reverse-phase HPLC. If this is done with and without prior reduction, it is possible to isolate and identify disulfide-linked peptides. Isolated disulfide-linked peptides can also be identified by plasma desorption mass spectroscopy. By such methods it has been demonstrated that all of the above-mentioned molecules have intrachain disulfide bonds linking Cys-4 and Cys-89, and linking Cys-43 and Cys-138.

EXAMPLE 28

Production and Characteristics of SCF
Analogues and Fragments Expressed in E. coli

5

Plasmid constructions for expression of numerous SCF analogs and fragments have been made. Site-directed mutagenesis has been used to prepare plasmids with initiating methionine codon followed by codons for amino acids 1 to 178, 173, 168, 166, 163, 162, 161, 160, 159, 158, 157, 156, 148, 145, 141, and 137, using the numbering of Figure 15C. The DNA for human SCF¹⁻¹⁸³ (Example 6B) was cloned into MP11 from XbaI to BamHI. Phage from this cloning was used to transfect an E. coli -
15 dut⁻ ung⁻ strain, R21032. Single stranded M13 DNA was prepared from this strain and site-directed mutagenesis was performed (reference IL-2 patent). After the site-directed mutagenesis reactions, the DNAs were transformed into an E. coli dut⁺ ung⁺ strain, JM101. Clones were
20 screened and sequenced as described in copending U.S. patent application Serial No. 717,334, filed March 29, 1985. Plasmid DNA preps were made from positive clones and the SCF regions from XbaI to BamHI were cloned into pCFM1656 as described in copending U.S.
25 patent application Serial No. 501,904, filed March 29, 1990. The oligonucleotides for each cloning were designed to substitute a stop codon for an amino acid codon at the appropriate position for each analog.

Plasmids with initiating methionine codon
30 followed by codons for amino acids 1 to 130, 120, 110, 100, 133, 127, and 123 (using the numbering of Figure 42) have been made using the polymerase chain reaction. The pCFM1156 human SCF¹⁻¹⁶⁴ plasmid DNA (Example 6B) was used to prime the reaction using a 5'
35 oligonucleotide 5' to the XbaI site and a 3' oligonucleotide which included a direct match to the

desired 3' end of the analog DNA, followed by a stop codon, followed by a BamH1 site. After the polymerase chain reaction, the polymerase chain reaction fragments were cleaved with Xba1 and BamH1, gel purified, and
5 cloned into pCFM1656 cut with Xba1 and BamH1.

Plasmids with initiating methionine codon followed by codons for amino acids 2 to 164, 5 to 164, and 11 to 164 (using the numbering of Figure 42) were also made using polymerase chain reaction. The pCFM1156
10 human SCF¹⁻¹⁶⁴ plasmid DNA (Example 6B) was used with two primers. The 5' oligonucleotide primer included an Nde1 site (which includes the ATG codon for the initiating methionine) and a homologous stretch of DNA starting at the codon for the first desired amino
15 acids. The 3' oligonucleotide primer was totally homologous and was 3' to the EcoR1 site in the gene. After the polymerase chain reaction, the fragment was cut with Nde1 and EcoR1, gel purified, and cloned back into the pCFM1156 human SCF¹⁻¹⁶⁴ plasmid cut with Nde1
20 and EcoR1.

A plasmid with initiating methionine codon followed by codons for amino acids 1 to 248 (using the numbering of Figure 42) was made using DNA obtained directly from the cDNA clone (Example 16). The cDNA was
25 cleaved with Spe1 and Dra1 (blunt end) and the fragment with the SCF region was gel purified. This was cloned into the pCFM1156 human SCF¹⁻¹⁸³ plasmid (Example 6B) which had been cut with HindIII, end filled with the Klenow fragment of DNA polymerase 1 (to yield a blunt
30 end), and then cut with Spe1 and gel purified. To allow for site-directed mutagenesis as above, the SCF¹⁻²⁴⁸ fragment was cloned into MP11 from Xba1 to BamH1; analog plasmids encoding initiating methionine followed by amino acids 1-189, 1-188, 1-185, or 1-180 (using
35 numbering of Figure 42) were then made using site-directed mutagenesis.

A plasmid with initiating methionine codon followed by codons for amino acids 1 to 220 (using the numbering of Figure 44) was made using DNA directly from the cDNA clone (Example 18), using the same methods
5 outlined in the preceding paragraph. Similarly, analog plasmids encoding initiating methionine followed by amino acids 1-161, 1-160, 1-157, or 1-152 (using the numbering of Figure 44) were made.

A pCFM1156 human SCF²⁻¹⁶⁵ plasmid was made by
10 cloning the XbaI to EcoRI SCF fragment from pCFM1156 human SCF²⁻¹⁶⁴ into the plasmid pCFM1156 human SCF¹⁻¹⁶⁵ (having synthetic codons; see Example 6B). Both DNAs were cut with XbaI and EcoRI and the fragments gel purified for cloning. The small fragment from pCFM1156
15 human SCF²⁻¹⁶⁴ was ligated to the large fragment of pCFM1156 human SCF¹⁻¹⁶⁵ (synthetic codons).

In considering the analog plasmids described above, it is noted that amino acids 4, 43, 89, and 138 are Cys in human SCFs, and the codons for Cys-4 or
20 Cys-138 are missing in certain of the plasmids described. Amino acids of the hydrophobic transmembrane region are at positions 190 (about) to 212 in the numbering of Figure 42, and positions 162 (about) to 184 in the numbering of Figure 44. Thus most of the
25 plasmids described encode amino acids that would be in the extracellular domain of membrane bound human SCF¹⁻²⁴⁸ (Figure 42 numbering) or human SCF¹⁻²²⁰ (Figure 44 numbering), and some include virtually all of these extracellular domains.

30 Plasmids encoding various other human SCF analogs and fragments can also be prepared by the methods described, and by other methods known to those skilled in the art. These include plasmids with codons for Cys residues replaced by codons for other amino
35 acids such as Ser.

E. coli host strain FM5 (Example 6) has been transformed with many of the analog plasmids described. These strains have been grown, with temperature induction, in flasks, and in fermentors as described in Example 6C.

After fermentation and harvesting of cells, many folded, oxidized, purified SCF analogs have been recovered by the methods outlined in Example 10. These include (by the numbering of Figure 42) SCF¹-189, SCF¹-188, SCF¹-185, SCF¹-180, SCF¹-156, SCF¹-141, SCF¹-137, SCF¹-130, SCF²-164, SCF⁵-164, SCF¹¹-164, and (by the numbering of Figure 44) SCF¹-161, SCF¹-160, SCF¹-157, SCF¹-152. Like SCF¹-164 and SCF¹-165 (Examples 17 and 27), these analogs are all dimeric in solution, as judged using gel filtration. Most of these have biological specific activities in the radioreceptor assay (Example 9) and UT-7 proliferation assay (Example 9) similar to those of SCF¹-164 and SCF¹-165 (Example 9). Some, such as SCF²-164 and SCF⁵-164 have lowered specific activities in the radioreceptor assay and/or UT-7 assay (30-80% of the values for SCF¹-164 and SCF¹-165) while others, such as SCF¹¹-164, have negligible specific activity in both assays. SCF¹-130 has lowered specific activity in both the radioreceptor assay (about 50% of the value for SCF¹-164) and the UT-7 assay (about 15% of the value for SCF¹-164). SCF¹-137 has full specific activity in the radioreceptor assay but lowered specific activity in the UT-7 assay (about 25% of the value for SCF¹-164 and SCF¹-165); this analog therefore may be preferable as an SCF antagonist in situations where it would be advantageous to block the biological activity of SCF.

While the present invention has been described in terms of preferred embodiments, it is understood that variations and modifications will occur to those skilled in the art. Therefore, it is intended that the appended
5 claims cover all such equivalent variations which come within the scope of the invention as claimed.

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WHAT IS CLAIMED IS:

1. A non-naturally-occurring polypeptide
having an amino acid sequence sufficiently duplicative
5 of that of naturally-occurring stem cell factor to allow
possession of a hematopoietic biological activity of
naturally occurring stem cell factor.

2. A purified polypeptide comprising
10 naturally-occurring stem cell factor.

3. A polypeptide according to Claim 1 or 2
wherein said polypeptide is the product of procaryotic
or eukaryotic expression of an exogenous DNA sequence.
15

4. A polypeptide according to Claim 3
wherein said polypeptide is the product of CHO cell
expression.

5. A polypeptide according to Claim 3
20 wherein the exogenous DNA sequence is a cDNA sequence.

6. A polypeptide according to Claim 1 or 2
wherein said stem cell factor is human stem cell factor.
25

7. A polypeptide according to Claim 3
wherein the exogenous DNA sequence is a genomic DNA
sequence.

8. A polypeptide according to Claim 3
30 wherein the exogenous DNA sequence is carried on an
autonomously replicating DNA plasmid or viral vector.

35

9. A polypeptide according to Claim 1
possessing part or all of the amino acid sequence of
human stem cell factor as set forth in Figure 15B,
Figure 15C, Figure 42 or Figure 44 or any naturally-
5 occurring allelic variant thereof.

10. A polypeptide according to Claim 1 which
has an in vivo biological activity of naturally-
occurring stem cell factor.

10

11. A polypeptide according to Claim 1 which
has an in vitro biological activity of naturally-
occurring stem cell factor.

15

12. A polypeptide according to Claim 1 or 2
further characterized by being covalently associated
with a detectable label substance.

13. An isolated DNA sequence for use in
20 securing expression in a procaryotic or eukaryotic host
cell of a polypeptide product having an amino acid
sequence sufficiently duplicative of that of naturally-
occurring stem cell factor to allow possession of a
hematopoietic biological activity of naturally occurring
25 stem cell factor, said DNA sequence selected from among:

(a) DNA sequences set out in Figure 14B,
Figure 14C, Figure 15B, Figure 15C, Figure 42,
Figure 44, or their complementary strands;

(b) DNA sequences which hybridize to the DNA
30 sequences defined in (a) or fragments thereof; and

(c) DNA sequences which, but for the
degeneracy of the genetic code, would hybridize to the
DNA sequences defined in (a) and (b).

35

14. A procaryotic or eukaryotic host cell transformed or transfected with a DNA sequence according to Claim 13 in a manner allowing the host cell to express said polypeptide product.

5

15. A polypeptide product of the expression of a DNA sequence of Claim 13 in a procaryotic or eukaryotic host cell.

10

16. An isolated DNA sequence coding for procaryotic or eukaryotic host expression of a polypeptide having an amino acid sequence sufficiently duplicative of that of naturally occurring stem cell factor to allow possession of a hematopoietic biological activity of naturally-occurring stem cell factor.

15

17. A cDNA sequence according to Claim 16.

20

18. A genomic DNA sequence according to Claim 16.

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19. A DNA sequence according to Claim 16 wherein said DNA sequence codes for human stem cell factor.

30

20. A DNA sequence according to Claim 19 and including one or more codons preferred for expression in E. coli cells.

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21. A DNA sequence according to Claim 16 having the sequence set out in Figure 15B, Figure 15C, Figure 42 or Figure 44.

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22. A DNA sequence according to Claim 16 and including one or more codons preferred for expression in yeast cells.

23. A DNA sequence according to Claim 16 covalently associated with a detectable label substance.

24. A DNA sequence coding for a polypeptide
5 fragment or polypeptide analog of naturally-occurring stem cell factor.

25. A DNA sequence as in Claim 24 coding for methionyl stem cell factor.
10

26. A biologically functional plasmid or viral DNA vector including a DNA sequence according to Claim 16.

27. A procaryotic or eukaryotic host cell
15 stably transformed or transfected with a DNA vector according to Claim 26.

28. A polypeptide product of the expression
20 in a procaryotic or eukaryotic host cell of a DNA sequence according to Claim 16.

29. A polypeptide having part or all of the amino acid sequence as set forth in Figure 15C,
25 Figure 42 or Figure 44 and having one or more of the in vitro biological activities of naturally-occurring stem cell factor.

30. A polypeptide having part or all of the
30 secondary conformation of naturally-occurring stem cell factor and having part or all of the amino acid sequence set forth in Figure 15C, Figure 42, or Figure 44 and having a biological property of naturally-occurring human stem cell factor.

35

31. A process for the production of stem cell factor comprising:

growing, under suitable nutrient conditions, procaryotic or eukaryotic host cells transformed or
5 transfected with a DNA according to Claim 13, and
isolating desired polypeptide products of the expression of DNA sequences in said vector.

32. A composition comprising a purified and
10 isolated human stem cell factor free of association with any human protein in glycosylated or nonglycosylated form.

33. A pharmaceutical composition comprising
15 an effective amount of a polypeptide according to Claim 1 and a pharmaceutically-acceptable diluent, adjuvant or carrier.

34. A method for treatment of leucopenia in a
20 mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

35. A method for treatment of
25 thrombocytopenia in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

36. A method for treating anemia in a mammal
30 comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

37. A method for enhancing engraftment of
35 bone marrow during transplantation in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

38. A method of enhancing bone marrow recovery in treatment of radiation, chemical, or chemotherapeutic induced bone marrow aplasia or myelosuppression which comprises treating patients with
5 therapeutically effective doses of stem cell factor.

39. A DNA sequence coding for an analog of human stem cell factor selected from the group consisting of:

- 10 a) [Met⁻¹] stem cell factor; and
 b) stem cell factor wherein one or more cysteines are replaced by alanine or serine.

40. A polypeptide product of the expression
15 in a procaryotic or eukaryotic host cell of a DNA sequence according to Claim 39.

41. A pharmaceutical composition comprising recombinant stem cell factor having the human amino acid
20 sequence, and a pharmaceutically acceptable diluent, adjuvant or carrier.

42. An antibody specifically binding stem cell factor.
25

43. An antibody as in Claim 42 wherein said antibody is a monoclonal antibody.

44. A process for the efficient recovery of
30 stem cell factor from SCF containing material, the method comprising the step of subjecting the SCF containing material to ion exchange chromatographic separation.

35

45. A process as in Claim 44 wherein said ion exchange chromatographic separation is anion exchange chromatographic separation.

5 46. A process as in Claim 44 further comprising the step of reverse phase liquid chromatographic separation.

10 47. A process for the efficient recovery of stem cell factor from SCF containing material, the method comprising the step of subjecting the SCF containing material to reverse phase liquid chromatographic separation.

15 48. A polypeptide having the hematopoietic biological activity of naturally occurring stem cell factor, said polypeptide having an amino acid sequence set forth in Figure 15C, Figure 42 or Figure 44 or any allelic variants, derivatives, deletion analogs,
20 substitution analogs, or addition analogs thereof, and characterized by being the product of procaryotic or eucaryotic expression of an exogenous DNA sequence.

25 49. A polypeptide as in Claim 48 selected from the group consisting of:
 SCF²-164, SCF⁵-164, SCF¹-130,
 SCF¹-148, SCF¹-162, SCF¹-164, SCF¹-165, SCF¹-183
 (Figure 15C); SCF¹-185, SCF¹-188, SCF¹-189, and SCF¹-248
 (Figure 42); and SCF¹-157, SCF¹-160, SCF¹-161 and
30 SCF¹-220 (Figure 44).

 50. A biologically active composition comprising the polypeptide of Claim 1 covalently attached to a water-soluble polymer.

51. A composition as in Claim 50 wherein said polymer is selected from the group consisting of polyethylene glycol or copolymers of polyethylene glycol and polypropylene glycol, and said polymer is
5 unsubstituted or substituted at one end with an alkyl group.

52. The composition of Claim 50 wherein the polypeptide is [Met⁻¹] SCF¹-164.
10

53. The composition of Claim 50 wherein said polymer has an average molecular weight of about 1,000 to 100,000 daltons.

54. The composition of Claim 50 wherein said
15 polymer has an average molecular weight of about 4,000 to 40,000 daltons.

55. The composition of Claim 50 wherein said
20 polymer is an unsubstituted polyethylene glycol or a monomethoxy polyethylene glycol.

56. The composition of Claim 50 wherein said polymer is attached to said polypeptide via reaction
25 with an active ester of a carboxylic acid or carbonate derivative of said polymer.

57. The composition of Claim 50 wherein one or more amino groups of said protein are conjugated to
30 said polymer by reaction with a N-hydroxysuccinimide, p-nitrophenol or 1-hydroxy-2-nitro-benzene-4-sulfonate ester of the polymer.

58. The composition of Claim 50 wherein one
35 or more free cysteine sulfhydryl groups are conjugated to said polymer via reaction with a maleimido or haloacetyl derivative of the polymer.

59. The composition of Claim 50 wherein the polypeptide is glycosylated and the polymer is attached by reaction of an amino, hydrazine or hydrazide derivative of the polymer with one or more aldehyde groups generated by oxidation of the carbohydrate moieties.

60. A method for preparing a biologically active polymer-polypeptide adduct which comprises reacting the polypeptide of Claim 50 with a water-soluble polymer under conditions permitting the covalent attachment of the polymer to said polypeptide, and recovering the adduct so produced.

61. A method of treating acquired immune deficiency in a human comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

62. A method of treating neoplasia in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

63. A method as in Claim 62 wherein before said administering step is the step of administering chemotherapy or irradiation to said mammal.

64. A method of transfecting early hematopoietic progenitor cells with a gene comprising:
(i) culturing early hematopoietic progenitor cells with SCF; and
(ii) transfecting the cultured cells of step (i) with a gene.

35

65. A method of transferring a gene to a mammal comprising the steps of:

(i) culturing early hematopoietic progenitor cells with SCF;

5 (ii) transfecting the cultured cells of step (i) with a gene; and

(iii) administering the transfected cells to said mammal.

10 66. A method of treating nerve damage in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

15 67. A method of treating infertility in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

20 68. A method of treating intestinal damage in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

25 69. A method of treating myeloproliferative disorder in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1 conjugated to a toxin.

30 70. A polypeptide as in Claim 48 selected from the group consisting of:
[Met⁻¹]SCF¹-148, [Met⁻¹]SCF¹-162,
[Met⁻¹]SCF¹-164, [Met⁻¹]SCF¹-165, [Met⁻¹]SCF¹-183
(Figure 15C); [Met⁻¹]SCF¹-185, [Met⁻¹]SCF¹-188,
35 [Met⁻¹]SCF¹-189, and [Met⁻¹]SCF¹-248 (Figure 42); and
[Met⁻¹]SCF¹-157, [Met⁻¹]SCF¹-160, [Met⁻¹]SCF¹-161 and
[Met⁻¹]SCF¹-220 (Figure 44).

STEM CELL FACTOR

ABSTRACT OF THE DISCLOSURE

5 Novel stem cell factors, oligonucleotides
encoding the same, and methods of production, are
disclosed. Pharmaceutical compositions and methods of
treating disorders involving blood cells are also
disclosed.

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15

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25

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A-175-CIP4

35

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Stem Cell Factor: Composition Claims

(iii) NUMBER OF SEQUENCES: 104

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(v) COMPUTER READABLE FORM:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu	Glu	Ile	Cys	Arg	Asn	Pro	Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr
1				5					10					15	
Lys	Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr
			20					25					30		
Val	Ala	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met
		35					40					45			
Val	Thr	His	Leu	Ser	Val	Ser	Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser
		50				55					60				
Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly
65					70					75				80	
Lys	Ile	Val	Asp	Asp	Leu	Val	Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Lys
			85						90					95	
Asn	Val	Lys	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro
			100					105					110		
Glu	Glu	Phe	Phe	Ser	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp
		115					120					125			

Phe	Met	Val	Ala	Ser	Asp	Thr	Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu
130						135					140				
Gly	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu
145					150					155					160
Pro	Pro	Val	Ala	Ala											
					165										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACRTTYTTNG GNGCRTTYTC YTCCAT

26

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION:12 and 15
- (D) OTHER INFORMATION: /mod_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AARAAYTCYT CNGGNGTRAA RTT

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTYYTCNGGYT TYTT

14

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGARGARA AYCCCCCAA RAAYGT

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCNAAYGAYT AYATGWTMAC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGNGGNARCA TRAANGGYTT

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCAKAARAT CTTYAAANCG ATC

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATTTTCAA TAGATCCATT GA

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAACTATGT CGCC

14

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTAGTCAAGC TGACTGATAA G

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCAACAA TGACTAGGCA A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCCAGAGTC AGTGTC

16

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAAGCTTG CCTTTCCTTA TGAAGAAGA

29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCCGCGGT TACGGTGGTA ACATGAAGGG CTTTGTGA

38

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATAAATGCA AGTGATAATC C

21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGTCGACC CGCGGAACTT TAAGTCCATG CAACAC

36

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACCCGCGGT TATGCAACAG GGGGTAACAT AAATGG

36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACCCGCGGT TAGGCTGCAA CAGGGGGTAA CATAAA

36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTAATGTTG AAGAAACC

18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATGGTAGTA CAATTGTCAG AC

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCTGACAAAT TGTACTACCA TC

22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAATTTAGTG ACGTCTTTTA CA

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAGATGAGT TTTCTTTCAC GCAC

24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAATCATTCA AGAGCCCAGA ACCC

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACATCCATC CCGGGGAC

18

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGCAATAT TTTAAGTCTC AAGAAGACC

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCGCCGCGGC TCCTATAGGT GCTAATTGG

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCACCCT GTTTGTGCTG GATCGCA

27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGTGTCTAGA CTTGTGTCTT CTTCATAAGG A

31

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCCCCHGG

10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT TTTTTTTTGG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTTTTTTTT TTTTTTTTAG

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTTTTTTTTT TTTTTTTTCG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTCGGCCGAT CAGGCCCCC CCCC

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT 30

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCCGGATAG GCCTCACNNN NNNT 24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGCCGGATAG GCCTCAC 17

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(660..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(720..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAAGTATCTT TCTATTGGCG AAGGACATGT TTTCCCATAA GTGGTAAACA AACTGTCTGC	60
ACATAATAAT TATCTTGCTG CCGTAAAGAT TAGGTAAAT TCTGCCTTCG ATCTAAAAAC	120
ACACCCTTCT GTCAATCCGA GGAGCAGTGT GCTAGTCTAG AGGTCTAAAT GAAGGCTCCT	180
TTCACGGTTG TATTTCTGCT CCCCAAATTG TCCACATTTA AAAGGAGAGT GCTTCTTTTC	240
AGCCTTAGGC TCTGAATTTT ATGCATTCTT CCATTTTCCG AGGTCCCCC CAAGTGATAA	300
TTCTGTTACA CGTTGCTACA AGTTCATCCC TAATTGCCGT CAAGAACTG ACTGTAGAAG	360
GCTTACCACA GACGTTGTAA CCGACAGTAA AGCCATTGAA AGAGTAATTC AACAGGATG	420
GAAGCCAGGA GTATTTTGTG GCTGTTGCTC TTTTCTTTT CAGTTTGGTG AGAGCAGCTT	480
GAATGCTTAA CATTTAAGCC ATCAGCTTAA AACAAAACAA AACAAAACAA AAAAAACCC	540
CGCTCTGGCA TATTTGCACT TAACACATAC GGTATAAGGT GTTACTGGTT TGCATAGTTC	600
TGGATTTTTT TTTTTTAAAA ACTGATGGAC ACCAAGAAAT GTTCTGTTC TTTGTTTAG	659
ACT TGG ATT ATC ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT	707
Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20 -15 -10 -5	
CTC GTC AAA ACT CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA	755
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	
1 5 10	
AAA GAC ATT ACA AAA CTG GTAAGTAAAG AATGATTTTG GCATCTATAA	803
Lys Asp Ile Thr Lys Leu	
15	
GTCTTCCCTG TGCTTGCTGA CCACATAGGT TCAGGGCACT CCCGACAGGA GTTCCCAGCT	863
TTCTAAGATA AGGAATCACT GTACGAGTCT GAAGTGCTTC TTCTGGGCAA ATGGGAGATG	923
CTTAGGTCAT GGAGGGTTTA TCTGTATAAC TGGCCCTTTG CACACCAACA AAGTGACTGA	983
CTGGCTTTTG CCTGTTACCT ACTGTCTCCA GTCCTGGGCA TGGTATATAC TTAGGCACCC	1043
AAGATTGGAT TTACAACTCA AGCATTATAT ATTGGACAAC ACGGGGTATG AGATATTAAT	1103
GATATGTCAG GTTGGATGGA TGAGTTTCTT CAAGAAATTC TCTTGATTTT ACTCACGTTT	1163
TCATTTCTTG GTCTCTGTAG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA	1213
Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	
20 25	
ACC CTC AAC TAT GTC GCC GGG ATG GAT GTT TTG GTATGTAGTC CACACACTTC	1266
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu	
30 35	
TGAGTTGCCT TTTAGTAGCT AATGGGTGAC CTGTGCTTAT TCACATTGAA GACATTATTT	1326

GCTCTTTGTC	TTTTTTAGAT	GTTGACCTAT	AATTTTTCCT	TCAAGCTGCT	GCTAAGATTA	1386
TCAGTGAGCA	TTTCAGTATG	TGTTTTAAGC	CTACTCATT	AAAGGAAATG	GCTCATCTTA	1446
GACGTAGCAA	CCGATGTAA	TTTTTCCCCA	GGCATCTCTC	AGAGGGACTT	GAATGTTAAA	1506
ATCATGTAA	ATTTCTCCT	TGGCTATGTT	ATTTCTCATG	GCTATGTTAT	TCCTATTCGT	1566
ATTTCATTTA	AAGGGACGGA	ATATTTATTG	TATTTCTGAA	CTTTTTCAGG	CATGCATCCG	1626
GGTCTTTGAA	TAAAACACTA	AGACTCCTTC	TAGTAATGTT	TGTAATCCTG	TCTGTATCGA	1686
ATGTCTTTGA	AAACGCAGTG	ACTAAGCCAT	AAATAATCTT	CCACAGAACG	TCCAGTGGTT	1746
CATGAACTTT	GTATGTGGGG	GTGGGGCAAG	AATTGTCTCA	CTATTGGTCA	AGGAAGAGAA	1806
GGTAAGGTAT	GCAAGGGTGG	TTTAATCTTC	TTCCGTGGAA	GGACAAAATC	ATCTATCATT	1866
TCCTCTGATC	TCTATGCATT	TGTTTGTTTT	GAAGTGAATC	TGACTTGAGC	AAGAGTTGGC	1926
GTCCTGTGTT	CTGAGGAAAC	TCTTTGTCTT	GCAGTCAGTG	ACTAAAAGTG	CTGAGAGATC	1986
TGAAGAGCAC	TCTGAATCTG	CCATATTTTT	AATAGATGCT	TTGTCTTCTC	TTTGAATTTT	2046
TTCCAG	CCT AGT CAT TGT TGG TTA CGA GAT ATG GTA ACA CAC TTA TCA					2094
	Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser					
	40	45	50			
GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC						2142
Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly						
55	60	65				
TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG AAA ATA GTG GAT GAC						2190
Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp						
70	75	80	85			
CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG GTAACCTGGT ATTCATCAGA						2243
Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys						
90	95					
ATTATTTTTC	TTATACTGAG	CTCATGATGA	GCAATTCACA	ACCACTTGTA	ATTCCAGCTC	2303
CAGAGGACAT	TATCCCCTCT	TTGGATGCCA	TAGGAATCTG	CTCTCAAATA	TGTAGATACC	2363
ACCTCTGCCA	CCTCAGCACA	TACATACACA	TAATTAAAAA	ATAGAAACAT	TAAAGGAGTT	2423
CCAATCAATC	CTTATTCTTT	TCTGTATTCA	GTATGCCAG	ATGTAAATTC	TAGGAATATG	2483
TTTTAAAGGC	TAATTCTTAT	TTTGTAATAA	GCAGCTTTAA	AATTCTTAAT	TGTTTTTTTCG	2543
GGTCACTTTA	TTGTCCTATT	GCCACGACAT	TGTCCTGTCC	CATTGTCTGT	TATTCCTTCT	2603
GTTTTGTTTA	TTGTTCCCTA	GTTACTTTGA	TCATGAGATT	GACCTGTTAC	CCGTTGTTAT	2663
TCTCTGTAGC	CATTTTGAGT	TGTGTCTATT	AGAACAGCTG	TTAAATTACT	TGAATCATTG	2723

AGGACATAGT CAATAATCTA TTATGCTGAT CCAGTCAAGT CTATGAGTTA TTTGAAAAC	2783
AGAATCTTTG TTAATTATTT GTTTGCTTGT TTGTTTGTTC ATTATTTGTC TAG AAT	2839
Asn	
GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT GAA	2887
Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu	
100 105 110	
GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC TTC	2935
Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
115 120 125	
ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA GGT	2983
Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu Gly	
130 135 140 145	
CCT GAG AAA G GTAAGGCTTT TAAGCATTTT TTGTTTAAAT GTACATAGAA	3033
Pro Glu Lys	
AGCCTGAACT TCTGTAAGCC TCTACTGCTG AATCAACTAA ATGTGTTGCT GTAGAAAGAA	3093
CGTGTGGGTT TTTCTGATAA AAACAAAAAG CAAATATCAA TGACTACCAA TGATTATTAT	3153
CTAGCTTGAG AGATATGCCC TAAGACAGCG ATTCTCGATA TTTCTAAATT AAAGAATTGT	3213
GTGATGGTGG CTCACATATT TTCTAACTGT GATATTTGCC AGGAGAGTAG AATAATGTTA	3273
TTCTTCATCC CCAGAATTCC TAAGATTTCA CGTCTCATGT CTTTTCATA AGGTTCAAAC	3333
TCTGAGACTT GAGTTCTGAG CCTCAGCAGG TCATTCTGAA TCCCCACTCT CCCCAGCTG	3393
GGTCCCTATG GGGGAACTAA CTTCAATTGCT TTCTTTTAAA ACATGACGAG TTACCAACAG	3453
CTCCTCGCTA TTATAAACAT GTTCCTAAGC ATGTCTGTGC ATGCAATAAG CCTTCACTCT	3513
ACAAGACAGT TATGGTGTAT CGCTTGACAA AACTGAGCAG CCAAGCTGAG TATGAAATAA	3573
TAATCTAGAC TTGGGAGGCA GACCCAGCAC CTACTGTGAT ATTGCACTTC GCCTTTGGGG	3633
GACTCTATGA TTCAAAAGTT CACCATGTAA CACTGACACA TTATTGCTTT CTATTTAG AT	3693
Asp	
TCC AGA GTC AGT GTC AGA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC	3741
Ser Arg Val Ser Val Arg Lys Pro Phe Met Leu Pro Pro Val Ala Ala	
150 155 160 165	
AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGTAAGTACA CATATCTGAT	3794
Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn	
170 175	
TTACTGCATG CATGGCTCCA AGTATCCTCT ATAGGAGTGT TGCATGGACT TAAAGTTTAT	3854

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AAATCACTAC TAATAATGCT GTTCTGTCAC TGTATTTCCT TGTATGGGCT TCCTGACAAT 3914
TAAATATCTG GTTTGTAGAA TCGGATCTCC TTAGAGGTTA AGATGACCAT GACAAAATTA 3974
GGCCAATCAA CTTTCTGCGA AGGTTATTTT AAATAAGGCA CGAAATTAAT TGAAGGAAAA 4034
AAAAATACAA GCAAGGCCTT ATTTTGAATC ATGGTAGGCT TAAAATAGAC TTTGTGGAGA 4094
ATGTCCCTGA TCAAAGTGGA GTTTTCAGAT TTCAAGTGCA TGTGCTAACT CTCCACAATG 4154
TCAAGGCTAT TTTCAGTTTT GTGTCTCCAT ATTTACTACT GCATGTTTGG AAATTTGCTG 4214
ATGCTGTTAG ATTACCTAAG AATGTATGTT GAAGAAGAAT GGACTTCTTT CCCTAAAATT 4274
TCTGTCCTCT TTGCCCAAGA ACCCACGTTT CTGGAAGACT ATCTTATTTT CATGTCTGTG 4334
CAATGATCAT TATAAAGATT ATTGAATATA CTGGAATAC TCTGGTTTCT GTTTTTACAG 4394
ATTCATAATA GCTTATTCAG TCTTTAAAGA AAGTTCTCTG AAGTCCATGC TTTAGAATGT 4454
TTCTCTATCA AAACCTTGACC TGGACCTTAA ATAAAGCTAT ATTTAGTCTT TTTATCCCTG 4514
AAAAATATAT TTCACAGTGT AGACATTTGA TATACATCTA AGGGAAGGAT GCTGCCAGAA 4574
TGCTCGGGCT GGCAGTCTAC AAAGTCCACT GCTCTCAGGA TGGACTTCTG AAAGCGGAAA 4634
TTGTGAACTG CATGCATATA ACATATCAGA TCCTCGAGC 4673

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(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro
-20          -15          -10          -5

Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val
          1          5          10

Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile
          15          20          25

Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp
          30          35          40

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu
          45          50          55          60

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Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	
				65					70					75		
Asp	Lys	Leu	Gly	Lys	Ile	Val	Asp	Asp	Leu	Val	Ala	Cys	Met	Glu	Glu	
		80						85					90			
Asn	Ala	Pro	Lys	Asn	Val	Lys	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Thr	Arg	
		95					100					105				
Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	Asn	Arg	Ser	Ile	Asp	
	110					115					120					
Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	Ser	Asp	Cys	Val	Leu	
125					130					135					140	
Ser	Ser	Thr	Leu	Gly	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Arg	Lys	
			145						150					155		
Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	Arg	Asn	Asp	Ser	
		160						165					170			
Ser	Ser	Ser	Asn													
		175														

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..844

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 101..844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGGATCGCA	GCGCTGCCTT	TCCTT	ATG	AAG	AAG	ACA	CAA	ACT	TGG	ATT	ATC		52			
			Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile					
			-25					-20								
ACT	TGC	ATT	TAT	CTT	CAA	CTG	CTC	CTA	TTT	AAT	CCT	CTC	GTC	AAA	ACT	100
Thr	Cys	Ile	Tyr	Leu	Gln	Leu	Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	
	-15				-10				-5							
CAG	GAG	ATC	TGC	AGG	AAT	CCT	GTG	ACT	GAT	AAT	GTA	AAA	GAC	ATT	ACA	148
Gln	Glu	Ile	Cys	Arg	Asn	Pro	Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	
1				5				10					15			

AAA CTG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA ACC CTC AAC TAT	196
Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr	
20 25 30	
GTC GCC GGG ATG GAT GTT TTG CCT AGT CAT TGT TGG TTA CGA GAT ATG	244
Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met	
35 40 45	
GTA ACA CAC TTA TCA GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA	292
Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser	
50 55 60	
AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG	340
Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly	
65 70 75 80	
AAA ATA GTG GAT GAC CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG	388
Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
85 90 95	
AAT GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT	436
Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro	
100 105 110	
GAA GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC	484
Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp	
115 120 125	
TTC ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA	532
Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu	
130 135 140	
GGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA	580
Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu	
145 150 155 160	
CCC CCT GTT GCA GCC AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT	628
Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn	
165 170 175	
AGG AAA GCC GCA AAG TCC CCT GAA GAC CCA GGC CTA CAA TGG ACA GCA	676
Arg Lys Ala Ala Lys Ser Pro Glu Asp Pro Gly Leu Gln Trp Thr Ala	
180 185 190	
ATG GCA CTG CCG GCT CTC ATT TCG CTT GTA ATT GGC TTT GCT TTT GGA	724
Met Ala Leu Pro Ala Leu Ile Ser Leu Val Ile Gly Phe Ala Phe Gly	
195 200 205	
GCC TTA TAC TGG AAG AAG AAA CAG TCA AGT CTT ACA AGG GCA GTT GAA	772
Ala Leu Tyr Trp Lys Lys Lys Gln Ser Ser Leu Thr Arg Ala Val Glu	
210 215 220	
AAT ATA CAG ATT AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA CAG	820
Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Gln	
225 230 235 240	

AAA GAG AGA GAG TTT CAA GAG GTG TAATT
Lys Glu Arg Glu Phe Gln Glu Val
245

849

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	-25	-20	-15	-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Gln	Glu	Ile	Cys	Arg	Asn	Pro	-5	1	5	
Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	10	15	20	
Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val	Ala	Gly	Met	Asp	Val	Leu	25	30	35	
Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met	Val	Thr	His	Leu	Ser	Val	Ser	40	45	50	55
Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	60	65	70	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly	Lys	Ile	Val	Asp	Asp	Leu	Val	75	80	85	
Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Lys	Asn	Val	Lys	Glu	Ser	Leu	Lys	90	95	100	
Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	105	110	115	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	120	125	130	135
Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu	Gly	Pro	Glu	Lys	Asp	Ser	Arg	140	145	150	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	155	160	165	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ala	Lys	Ser	Pro	170	175	180	

Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile
185 190 195
Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys
200 205 210 215
Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
220 225 230
Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu
235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152
..3307, 3513..3595)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152
..3307, 3513..3595)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACAAGTGAG TAGGGCGCGC CCGGGAGCTC CCAGGCTCTC CAGGAAAAAT CGCGCCCGGT	60
GCCCCGGGGA AGCCGGCGCT CCCTGGGACT TGCAGCTGGG GCGTGCAGGG CTGTGCCTGC	120
CGGGTGAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT ACAGTGTAAT	180
AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT GTTATTTTCA	240
AGCCGATGTG TAGGTTATGT GTGTTGAGAG GAGAGAGAGA GAAGACAGAT TACTTTCTGC	300
TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT GGCTAAAAAG	360
CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGAATTCTC TTAGGTCTAA	420
AAATATACAT CTCTCTCACT TTAAGTTGGT GTGCTATTGT AGATTATTGG ATTAAAGCAC	480
TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA AATAAGATGT	540
TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA AGATACCCTA	600

AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG GGAAATTGGC	660
TGAAGAAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT TCAAAATGGA	720
TTTTAACTAA AAGCTTTTAA AAACCTTTGGT GAGCATAGCT TGAATGCGTA ATATTTAATT	780
GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTTGT GCATCAAGGC ATTAGATGTT	840
AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT CTGTTTTTCAT	900
TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT	949
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn	
-20 -15 -10	
CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT	997
Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn	
-5 1 5 10	
GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC CGTGCTGTGT	1048
Val Lys Asp Val Thr Lys Leu	
15	
AAAAAAGAGC TGTGGCTCTT TTTCTGTGC TTGTTGATAA AAGATTTAGA TTTTCTTGC	1108
CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT AAAGGGTTTA	1168
TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA ACTGGCTAGT	1228
TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC ATAGGCAGTG	1288
AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT CCCATAATC	1348
TCTCCAGTGG GTTCCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA CTCTTCTTTA	1408
AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA GCAGGAAGAC	1468
CCTGTCACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG ATTCATTGCC	1528
CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC TCAGCGAAAG	1588
CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC AGATCATGTT	1648
TCCAAAACCTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC TAAAAGATCT	1708
GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTTGATTA CAGAGGGAAA TCAAGGATTA	1768
AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC ACAACAGTTT	1828
TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA ATTTTCTTAT	1888
GGAATTTTTT TTTTGTCTC TG TAG GTG GCA AAT CTT CCA AAA GAC TAC ATG	1940
Val Ala Asn Leu Pro Lys Asp Tyr Met	
20 25	

ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG GTATGTAAAC	1986
Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
30 35	
TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTG ATATTGAGAT	2046
AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA TTTATCTTTG	2106
GAATTTGACT TGCAGGCTTT TTTTTCCTCT TCTTCCTGTT ACAAGAGTCC CTCCTCCTAT	2166
TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTGTGTA CAATAACCCC	2226
TGTCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC TGGCCAGGCA	2286
CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG ATCATTGAG	2346
GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC TAAAAATAAA	2406
AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG GCTGAGGCAG	2466
GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT TTATGGCACT	2526
TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTTCATATCT TGCAG CCA AGT CAT	2580
Pro Ser His	
40	
TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT	2628
Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp	
45 50 55	
CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC	2676
Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser	
60 65 70	
ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG	2724
Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val	
75 80 85 90	
AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	2772
Lys Glu Asn Ser Ser Lys	
95	
ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	2832
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTTCAGA TGAGCAAAGA	2892
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC ATTCTTGTGT TCACTGCCCC	2952
AGATTCAACT TGTGATCCCA CTGGGATCAC TACCCTGCAT TACCAATCTG AATTACATAC	3012
GTTAAAACAG CCATCTAAAA GTGCTAGTTG TAAGAGTCTA AATACTTGAA TCTTTGAGAG	3072
ACATATTTAT AGTCCATTAT CTTACCTCA GTTAAGTCTG AAGACTATTT GAAAAATGTA	3132

ATCCTATTTT TTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC	3184
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro	
100 105	
AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT	3232
Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile	
110 115 120	
GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG	3280
Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val	
125 130 135	
GTT TCT TCA ACA TTA AGT CCT GAG AAA GGTAAGACAT GTAAGCATT	3327
Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CCAGTTCAAA TGTAACAAC AAACCTAAAT CTTCCCTATG TAGTAAGAAT CTACCTCTGT	3387
GTTAAGCTGT AGCAAGATAC ATGCATGTAC GTCTAATAAA AAAGCAGATA TCAATAGCAC	3447
AGAAGAACT CTATAACTCA TACAAATCAC CATATAACAC TGACACATTA TTGCTTTCTA	3507
TTTAG ATT CCA GAG TCA GTG TCA CAA AAC CAT TTA TGT TAC CCC CTG	3554
Ile Pro Glu Ser Val Ser Gln Asn His Leu Cys Tyr Pro Leu	
150 155 160	
TTG CAG CCA GCT CCC TTA GGA ATG ACA GCA GTA GCA GTA ATAGTAAGTA	3603
Leu Gln Pro Ala Pro Leu Gly Met Thr Ala Val Ala Val	
165 170 175	
CATATATCTG ATTTAATGCA TGCATGGCTC CAATTAGCAC CTATAGGAGT ATTGCATGGG	3663
CTTCAAGGA AACTTCTACA TTTATTATTA TTGATACTGT TCTGTTACTG TTATTCCTTT	3723
TATGGTCTTC TTGAGACTTA AGTTTGTAGA ATTAAATTTC CCTAGAGCTG GAGATAATGT	3783
TTAGAGAATT AGGCCAATAA ATTT	3807

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20 -15 -10 -5	
Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val	
1 5 10	

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Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile
    15                      20                      25

Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp
    30                      35                      40

Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu
    45                      50                      55                      60

Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile
                      65                      70                      75

Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu
                      80                      85                      90

Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg
                      95                      100                      105

Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp
    110                      115                      120

Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
    125                      130                      135                      140

Ser Ser Thr Leu Ser Pro Glu Lys Ile Pro Glu Ser Val Ser Gln Asn
                      145                      150                      155

His Leu Cys Tyr Pro Leu Leu Gln Pro Ala Pro Leu Gly Met Thr Ala
                      160                      165                      170

Val Ala Val
    175

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(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 17..640

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 92..640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAGCTTGCCT TTCCTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC	49
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys	
-25 -20 -15	
ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG	97
Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly	
-10 -5 1	
ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG	145
Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
5 10 15	
GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC	193
Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro	
20 25 30	
GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA	241
Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val	
35 40 45 50	
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT	289
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile	
55 60 65	
TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA	337
Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile	
70 75 80	
GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA	385
Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu	
85 90 95	
AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA	433
Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu	
100 105 110	
TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA	481
Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val	
115 120 125 130	
GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT	529
Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro	
135 140 145	
GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT	577
Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro	
150 155 160	
GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGT AAG	625
Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys	
165 170 175	
TAC ATA TAT CTG ATT TAATGCATGC ATGGCTCCAA TTAGCACCTA TAGGAGTATT	680
Tyr Ile Tyr Leu Ile	
180	

GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG ATACTGTTCT GTTACTGTTA 740
TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT AAATTTCCCT AGAGCTGGAG 800
ATAATGTTTA GAGAATTAGG 820

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25 -20 -15 -10
Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
-5 1 5
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
10 15 20
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
25 30 35
Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
40 45 50 55
Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
60 65 70
Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
75 80 85
Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
90 95 100
Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
105 110 115
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
120 125 130 135
Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
140 145 150
Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
155 160 165
Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys Tyr Ile Tyr Leu Ile
170 175 180

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAGCTCCGAG CCCTCTCTGG CGCGCGAGGT ATTTCTGTCTG TNCCCGGGGG TGCCAGGTGA	60
GGCCAGCGG ATCCGGGAGG GTAAGCTGGG ACTCCTCGCG AGCAGTAGCT GCAGGGTACC	120
AAGCTTCGCC CTCTGCGTCC CCGCGCCTTC GCGGTCTCCC GCCAGTGCAG GTCCGGGGCC	180
CCCAGGCGAG CGGACAAGGT TGGCCTAATC TGCCAACTT CTGGGGCATT TACCGTGCTC	240
TGGCCGCCCT CCCGATTCTT CCCTCCGCGC CTTGCTGCTG TTCTCGCCTA CCCCGGGCTC	300
CGGAAGGGAA GGAGGCGTGT CCGGAGCAGG CGGGCGGGAA CTGTATAAAA GCGCCGGCGG	360
CTCAGCAGCC GGCTTCGCTC GCGCCTCGC GCGGAGACTA GAAGCGCTGC GGGAAGCAGG	420
GACAGTGGAG AGGGCGCTGC GCTCGGGCTA CCCAATGCGT GGAATATCTG CCGCCGCTGT	480
TCGTGCAATA TGCTGGAGCT CCAGAACAGC TAAACGGAGT CGCCACACCA CTGTTTGTGC	540
TGGATCGCAC CGCTGCCTTT CTT ATG AAG AAG ACA CAA GTGAGTAGGG	589
Met Lys Lys Thr Gln	
-25	
CGCGCCCGGG AGCTCCAGG CTCTCCAGGA AAAATCGCGC CCGGTGCCCC GGGGAAGCCG	649
GCGCTCCCTG GGAATTGCAG CTGGGGCGTG CAGGGCTGTG CCTGCCGGGT GAGACAAGAG	709
GATGCGGGGG AGGCCGGCGT GGTGTGTGAT CCCGAGCCGA GCCGNNTGAG CCAGGGAGAA	769
AAGGAGTGGG AGTACTGAGA GGGAGCCAGT GTCAAGTTTG GAGCCTCAGC AGTTAAGTTT	829
TGAGCTGTCA GTCGGAACC GTAATTCCCG TCTGGTGGAA AGATTGGCTT TTNGNCCACG	889

GAATGTAAGT TATCACAGAT ACTACAAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT	949
ACAGTGTAAT AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT	1009
GTTATTTTCA AGCCGATGTG TAGGTTATGT GTGTTTCGAGA GAGAGAGAGA GAAGACAGAT	1069
TACTTTCTGC TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT	1129
GGCTAAAAAG CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGGAATTCTC	1189
TTAGGTCTAA AAATATACAT CTCTCTCACT TTAAGTTGGT GTGCTATTGT AGATTATTGG	1249
ATTAAAGCAC TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA	1309
AATAAGATGT TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA	1369
AGATACCCTA AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG	1429
GGAAATTGGC TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT	1489
TCAAAATGGA TTTTAACTAA AAGCTTTTAA AAAGTTTGGT GAGCATAGCT TGAATGCGTA	1549
ATATTTAATT GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTTGT GCATCAAGGC	1609
ATTAGATGTT AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT	1669
CTGTTTTTCAT TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC	1719
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu	
-20 -15 -10	
CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG	1767
Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val	
-5 1 5	
ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC	1817
Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
10 15	
CGTGCTGTGT AAAAAAGAGC TGTGGCTCTT TTTCTGTGCT TTGTTGATAA AAGATTTAGA	1877
TTTTTCTTGC CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT	1937
AAAGGGTTTA TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA	1997
ACTGGCTAGT TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC	2057
ATAGGCAGTG AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT	2117
CCCATAATC TCTCCAGTGG GTTTCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA	2177
CTCTTCTTTA AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA	2237
GCAGGAAGAC CCTGTCACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG	2297
ATTCATTGCC CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC	2357

TCAGCGAAAG CATTTCGATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC	2417
AGATCATGTT TCCAAAACCTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC	2477
TAAAAGATCT GTATTATCAC TTTTATTATTT TGAAGGATGC CTTTGTGATTA CAGAGGGAAA	2537
TCAAGGATTA AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC	2597
ACAACAGTTT TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA	2657
ATTTTCTTAT GGAATTTTTT TTTTGTCTC TGTAG GTG GCA AAT CTT CCA AAA	2710
Val Ala Asn Leu Pro Lys	
20	
GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG	2755
Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
25 30 35	
GTATGTAAAC TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC	2815
ATATTGAGAT AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA	2875
TTTATCTTTG GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCCTGTT ACAAGAGTCC	2935
CTCCTCCTAT TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTCTGTTA	2995
CAATAACCCC TGCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC	3055
TGGCCAGGCA CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG	3115
ATCATTTGAG GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC	3175
TAAAAATAAA AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG	3235
GCTGAGGCAG GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT	3295
TTATGGCACT TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA	3353
Pro	
40	
AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG	3401
Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu	
45 50 55	
ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT	3449
Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn	
60 65 70	
TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG	3497
Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu	
75 80 85	
TGC GTG AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	3551
Cys Val Lys Glu Asn Ser Ser Lys	
90 95	

ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	3611
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTTCTG TGAGCAAAGA	3671
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC TATTCTTGTG TTCACTGCCC	3731
CAGATTCAAC TTGTGATCCC ACTGGGATCA CTACCCTGCA TTACCAATCT GAATTACATA	3791
CGTTAAAACA GCCATCTAAA AGTGCTAGTT GTAAGAGTCT AAATACTTGA ATCTTTGAGA	3851
GACATATTTA TAGTCCATTA TCTTCACCTC AGTTAAGTCT GAAGACTATT TGAAAAATGT	3911
AATCCTATTT TTTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA	3961
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu	
100 105	
CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC	4009
Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser	
110 115 120	
ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT	4057
Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys	
125 130 135	
GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA G GTAAGACATG TAAGCATTTT	4108
Val Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CAGTTCAAAT GTAAACAACA AACTTAAATC TTCCCTATGT AGTAAGAATC TACCTCTGTG	4168
TTAAGCTGTA GCAAGATACA TGCATGTACG TCTAAAAAAA AGCAGATATC AATAGCACAG	4228
AAGAACTAA TGATTGTAGA TTTGTGGGCT CTATAACTCA TACAAATCAC CATATAACAC	4288
TGACACATTA TTGCTTTCTA TTTAG AT TCC AGA GTC AGT GTC ACA AAA CCA	4339
Asp Ser Arg Val Ser Val Thr Lys Pro	
150 155	
TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT	4387
Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser	
160 165 170	
AGC AGT AAT A GTAAGTACAT ATATCTGATT TAATGCATGC ATGGCTCCAA	4437
Ser Ser Asn	
175	
TTAGCACCTA TAGGAGTATT GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG	4497
ATACTGTTCT GTTACTGTTA TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT	4557
AAATTTCCCT AGAGCTGGAG ATAATGTTTA GAGAATTAGG CCAATAAATT TTCTGCTGAG	4617
GTTATTTTAA ATAAGACATA AAATTAATTT TAGAAATATG ATTTATGCCT TTTGTTGAAT	4677
CATTAACATA TATACAGAAA CAGTTAAAAC AACCACAGCA TAAGAGAAAA ACTTCTAGAA	4737

TGGATATGCT GTATTCATCA GTGTGTTCTT TAAATTATAG	GG AAG GCC AAA AAT	4791
	Arg Lys Ala Lys Asn	
	180	
CCC CCT GGA GAC TCC AGC CTA CAC TGG CCA GCC ATG GCA TTG CCA GCA	4839	
Pro Pro Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala		
185 190 195		
TTG TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG	4887	
Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys		
200 205 210		
GTAAGTGGTA CCATTCCTTT TTTTAAAAAT ATGCTATGTT TACATAAATT ATCATCTTTT	4947	
TTTCCTCAAG AAATGATCCT TTAAGAAAAC AGTGAATCTA CCTTAGCTTA TACTAAACAA	5007	
AATTTAAATT TTATAAAGTT TCCTGTTTCT CATTATGTCT GGAGACAATC CCTCTAGCTG	5067	
ATAATTCACG CTTAAGAATT AGGAACTAAA ACTGTTATTG GAGTTATTGC CATAAAAGAT	5127	
AAAAGTGGAG TCCACTTACC TCTTAAATAT TAGACCATTC ATTGATTATT TTACAGTATA	5187	
TGTCTTTCTT CTTTTTCCAG AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT	5237	
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val		
215 220		
GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA AG GTATTTTGT	5285	
Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser		
225 230 235		
TTGCTAAATG TGTGCCCAAT CAAGCATGAC ATTGCCATTT CACACACTGT GTACCTGCCC	5345	
ATAATGTCTT TAAGAAGTCC TTCACTCATG ACAGTAGCTC CTAACCAGTG AGTCCCAACT	5405	
CTATCCATGT TTCTGATGTC TCACTCTCTC TTCGTATGTG TATATGCATA TACAGAGAAA	5465	
GAAATGTTTT AACTACTTGG AAAGACTACC TTAAGACAAA TGAAGTCTTC CCTCTTCCCT	5525	
ATAGTAATAA GAAGGTAGGC TCCCCATTC AATTTTGCAA TCTTCTGCTA CTATATTTAC	5585	
AGAAAAGCTG CCTTTTACAA TGCCGAGATC ATGGTGTACC TCAGAATCTC TGACCAAGAG	5645	
CAAATAAGCA TTTTTTCTTA TTGTTTTTCA G T ATG TTG CAA GAG AAA GAG AGA	5698	
Met Leu Gln Glu Lys Glu Arg		
240		
GAG TTT CAA GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG	5753	
Glu Phe Gln Glu Val		
245		
GTAAGTTTTT TTCTTCTTTC CTTTTTTTTT CTTTTTTTTT TTATACTTTA AGTTCTAGGG	5813	
TACATGTGCA CAATGTGCAG GTTTGTTACG TATGTTTACA TGTGCCATGT T	5864	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

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Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25                      -20                      -15                      -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
                      -5                      1                      5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
          10                      15                      20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
          25                      30                      35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
          40                      45                      50                      55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
                      60                      65                      70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
          75                      80                      85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
          90                      95                      100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
          105                      110                      115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
          120                      125                      130                      135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
          140                      145                      150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
          155                      160                      165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
          170                      175                      180

Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala Leu Phe
          185                      190                      195

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
          200                      205                      210                      215

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Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
220 225 230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
20 25 30

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
100 105 110

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
115 120 125

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
145 150 155 160

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
180 185 190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
 195 200 205

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe
 210 215 220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
 225 230 235 240

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
 245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
 260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
 1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
 20 25 30

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
 35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
 50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
 65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
 85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
 100 105 110

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
 115 120 125

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
 130 135 140

```

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Ala Val Ala Ser Glu Thr
145                      150                      155                      160

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
                      165                      170                      175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
                      180                      185                      190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Thr
                      195                      200                      205

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Phe Phe
210                      215                      220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
225                      230                      235                      240

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
                      245                      250                      255

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
260                      265                      270

Val

```

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1                      5                      10                      15

Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Gly Ile Cys Gly Lys Arg
20                      25                      30

Val Thr Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
35                      40                      45

Lys Asp Tyr Lys Ile Ala Leu Lys Tyr Val Pro Gly Met Asp Val Leu
50                      55                      60

Pro Ser His Cys Trp Ile Ser Val Met Val Glu Gln Leu Ser Val Ser
65                      70                      75                      80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85                      90                      95

```

```

Asn Tyr Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val
      100                      105                      110

Glu Cys Thr Glu Gly Tyr Ser Phe Glu Asn Val Lys Lys Ala Pro Lys
      115                      120                      125

Ser Pro Glu Leu Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
      130                      135                      140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Leu Glu Thr Val Ala Ser Lys
      145                      150                      155                      160

Ser Ser Glu Cys Val Val Ser Ser Thr Leu Ser Pro Asp Lys Asp Ser
      165                      170                      175

Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser
      180                      185                      190

Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser
      195                      200                      205

Ile Gly Asp Ser Asn Leu Gln Trp Ala Ala Met Ala Leu Pro Ala Phe
      210                      215                      220

Phe Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys
      225                      230                      235                      240

Lys Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Ile Gln Ile Asn Glu
      245                      250                      255

Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln
      260                      265                      270

Glu Val

```

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Met Lys Thr Gln Thr Trp Ile Val Thr Cys Ile Tyr Leu Gln Leu Leu
 1              5              10              15

Phe Asn Pro Leu Val Lys Thr Lys Gly Leu Cys Arg Asn Arg Val Thr
      20              25              30

Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp
      35              40              45

```

Tyr	Lys	Ile	Ala	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	50	55	60	
His	Cys	Trp	Ile	Ser	Val	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	Leu	Thr	65	70	75	80
Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	85	90	95	
Ser	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	100	105	110	
Val	Glu	Gly	His	Ser	Ser	Glu	Asn	Val	Lys	Lys	Ser	Ser	Lys	Ser	Pro	115	120	125	
Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	130	135	140	
Ser	Ile	Asp	Ala	Phe	Lys	Asp	Leu	Glu	Met	Val	Ala	Ser	Lys	Thr	Ser	145	150	155	160
Glu	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	165	170	175	
Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	180	185	190	
Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Thr	Asn	Pro	Ile	Glu	Asp	195	200	205	
Ser	Ser	Ile	Gln	Trp	Ala	Val	Met	Ala	Leu	Pro	Ala	Cys	Phe	Ser	Leu	210	215	220	
Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Phe	Tyr	Trp	Lys	Lys	Lys	Gln	Pro	225	230	235	240
Asn	Leu	Thr	Arg	Thr	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	Asp	Asn	245	250	255	
Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	Val	260	265	270		

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val His Thr Gln Gly Ile Cys Ser Asn Arg
20 25 30

Val Thr Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Glu Gln Leu Ser Val Ser
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85 90 95

Asn Tyr Cys Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val
100 105 110

Glu Cys Met Glu His Ser Ser Glu Asn Val Lys Lys Ser Ser Lys Ser
115 120 125

Pro Glu Pro Arg Gln Phe Thr Pro Glu Lys Phe Phe Gly Ile Phe Asn
130 135 140

Lys Ser Ile Asp Ala Phe Lys Asp Leu Glu Ile Val Ala Ser Lys Met
145 150 155 160

Ser Glu Cys Val Ile Ser Ser Thr Ser Ser Pro Glu Lys Asp Ser Arg
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
180 185 190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser Ile
195 200 205

Glu Asp Ser Ser Leu Gln Trp Ala Ala Val Ala Leu Pro Ala Phe Phe
210 215 220

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Phe Tyr Trp Lys Lys Lys
225 230 235 240

Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Arg Gln Ile Asn Glu Glu
245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1           5           10           15

Leu Leu Phe Asn Pro Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro
          20           25           30

Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro
          35           40           45

Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu
50           55           60

Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser Val Ser
65           70           75           80

Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
          85           90           95

Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val
          100          105          110

Ala Cys Met Glu Glu Asn Ala Pro Leu Asn Val Lys Glu Ser Leu Lys
          115          120          125

Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe
          130          135          140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr
          145          150          155          160

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg
          165          170          175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
          180          185          190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ser Pro
          195          200          205

Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile
          210          215          220

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys
          225          230          235          240

```

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu
260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Glu Ile Cys Gly Asn Pro
20 25 30

Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro
35 40 45

Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu
50 55 60

Pro Ser His Cys Trp Leu Arg Asp Met Val Ile Gln Leu Ser Leu Ser
65 70 75 80

Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val
100 105 110

Leu Cys Met Glu Glu Asn Ala Pro Lys Asn Ile Lys Glu Ser Pro Lys
115 120 125

Arg Pro Glu Thr Arg Ser Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr
145 150 155 160

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
180 185 190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ala Pro
 195 200 205

Glu Asp Ser Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile
 210 215 220

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys
 225 230 235 240

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
 245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu
 260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr Trp Ile Ile Thr Cys Phe Cys Leu Gln Leu Leu Leu Leu Asn Pro
 1 5 10 15

Leu Val Lys Ala Gln Ser Ser Cys Gly Asn Pro Val Thr Asp Asp Val
 20 25 30

Asn Asp Ile Ala Lys Leu Val Gly Asn Leu Pro Asn Asp Tyr Leu Ile
 35 40 45

Thr Leu Lys Tyr Val Pro Lys Met Asp Ser Leu Pro Asn His Cys Trp
 50 55 60

Leu His Leu Met Val Pro Glu Phe Ser Arg Ser Leu His Asn Leu Leu
 65 70 75 80

Gln Lys Phe Ser Asp Ile Ser Asp Met Ser Asp Val Leu Ser Asn Tyr
 85 90 95

Ser Ile Ile Asn Asn Leu Thr Arg Ile Ile Asn Asp Leu Met Ala Cys
 100 105 110

Leu Ala Phe Asp Lys Asn Lys Asp Phe Ile Lys Glu Asn Gly Leu His
 115 120 125

Tyr Glu Glu Asp Arg Phe Ile Pro Glu Asn Phe Phe Arg Leu Phe Asn
 130 135 140


```

Ser Thr Ile Glu Val Tyr Lys Glu Phe Ala Asp Ser Leu Asp Lys Asn
145                      150                      155                      160

Asp Cys Ile Met Pro Ser Thr Val Glu Thr Pro Glu Asn Asp Ser Arg
                      165                      170                      175

Val Ala Val Thr Lys Thr Ile Ser Phe Pro Pro Val Ala Ala Ser Ser
                      180                      185                      190

Leu Arg Asn Asp Ser Ile Gly Ser Asn Thr Ser Ser Asn Ser Asn Lys
                      195                      200                      205

Glu Ala Leu Gly Phe Ile Ser Ser Ser Ser Leu Gln Gly Ile Ser Ile
                      210                      215                      220

Ala Leu Thr Ser Leu Leu Ser Leu Leu Ile Gly Phe Ile Leu Gly Ala
225                      230                      235                      240

Ile Tyr Trp Lys Lys Thr His Pro Lys Ser Arg Pro Glu Ser Asn Glu
                      245                      250                      255

Thr Ile Gln Cys His Gly Cys Gln Glu Glu Asn Glu Ile Ser Met Leu
                      260                      265                      270

Gln Gln Lys Glu Lys Glu His Leu Gln Val
                      275                      280

```

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
1                      5                      10                      15

Leu Leu Phe Asn Pro Leu Val Lys Thr Gly Ile Cys Arg Asn Arg Val
                      20                      25                      30

Thr Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp
                      35                      40                      45

Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser
50                      55                      60

His Cys Trp Ile Ser Glu Met Val Glu Gln Leu Ser Val Ser Leu Thr
65                      70                      75                      80

```

Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr			
				85					90					95				
Ser	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys			
			100				105						110					
Glu	Glu	Asn	Ser	Ser	Lys	Asn	Val	Lys	Lys	Ser	Lys	Ser	Pro	Glu	Pro			
		115				120						125						
Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile			
	130					135					140							
Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Lys	Thr	Ser	Asp	Cys	Val			
145					150				155					160				
Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr			
				165				170					175					
Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	Arg	Asn	Asp			
			180				185						190					
Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Asn	Glu	Asp	Ser	Ser	Leu	Gln	Trp			
	195					200						205						
Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	Ser	Leu	Val	Ile	Gly	Phe	Ala			
	210					215					220							
Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Lys	Gln	Pro	Ser	Leu	Thr	Arg	Ala			
225					230					235				240				
Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	Asp	Asn	Glu	Ile	Ser	Met	Leu			
			245					250					255					
Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	Val									
		260					265											

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..210, 223..258)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAA	TTC	TTC	CGT	ATC	TTC	AAC	CGT	TCC	ATC	GAC	GCT	TTC	AAA	GAC	TTC
Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe
1					5				10				15		

GTT GTT GCT TCC GAA ACC TCC GAC TGC GTT GTT TCC TCC ACC CTG TCT	96
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
CCG GAA AAA GAC TCC CGT GTT TCG GTT ACC AAA CCG TTC ATG CTG CCG	144
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
CCG GTT GCT GCT TCC TCC CTG CGT AAC GAC TCC TCC TCC TCC AAC TCC	192
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
AAA TAC ATC TAC CTG ATC TAATAGGATC CG GTT ACC AAA CCG TTC ATG	240
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met	
65 70 75	
CTG CCG CCG GTT GCT GCT TAATAGGATC C	269
Leu Pro Pro Val Ala Ala	
80	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
1 5 10 15	
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met Leu Pro Pro Val	
65 70 75 80	
Ala Ala	

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 184..1002

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 259..1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGCCTCGCG CCGAGACTAG AAGCGCTGCG GGAAGCAGGG ACAGTGGAGA GGGCGCTGCG	60
CTCGGGCTAC CCAATGCGTG GACTATCTGC CGCCGCTGTT CGTGCAATAT GCTGGAGCTC	120
CAGAACAGCT AAACGGAGTC GCCACACCAC TGTTTGTGCT GGATCGCAGC GCTGCCTTTC	180
CTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG	228
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln	
-25 -20 -15	
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT	276
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn	
-10 -5 1 5	
CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA AAT CTT	324
Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu	
10 15 20	
CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT	372
Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val	
25 30 35	
TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC	420
Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp	
40 45 50	
AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG	468
Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu	
55 60 65 70	
AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT	516
Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu	
75 80 85	
GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA AAA AAA TCA TTC	564
Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe	
90 95 100	
AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT	612
Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile	
105 110 115	

TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA	660
Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu	
120 125 130	
ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC	708
Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser	
135 140 145 150	
AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC	756
Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser	
155 160 165	
TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC	804
Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro	
170 175 180	
CCT GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG	852
Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu	
185 190 195	
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG	900
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys	
200 205 210	
AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA	948
Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu	
215 220 225 230	
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA	996
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln	
235 240 245	
GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA	1052
Glu Val	
GTTCATGTTT GCTTCATAAA TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA	1112
CAGACCACAT CTTTATCTGT TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG	1172
GAACAGAATG TTTTACTGTG AAAGTGGCAC TGAATTAATC ATCTATAAAG AAGAACTTGC	1232
ATGGAGCAGG ACTCTATTTT AAGGACTGCG GGAAGTGGGT CTCATTTAGA ACTTGCAGCT	1292
GATGTTGGAA GAGAAAGCAC GTGTCTCAGA CTGCATGTAC CATTTCATG GCTCCAGAAA	1352
TGTCTAAATG CTGAAAAAAC ACCTAGCTTT ATTCTTCAGA TACAAACTGC AG	1404

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25 -20 -15 -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
-5 1 5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
10 15 20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
25 30 35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
40 45 50 55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
60 65 70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
75 80 85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
90 95 100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
105 110 115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
120 125 130 135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
140 145 150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
155 160 165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
170 175 180

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe
185 190 195

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
200 205 210 215

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
220 225 230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 151..885

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 226..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCAGGGACA GTGGAGAGGG CGCTGCGCTC GGGCTACCCA ATGCGTGGAC TATCTGCCGC	60
CGCTGTTCGT GCAATATGCT GGAGCTCCAG AACAGCTAAA CGGAGTCGCC ACACCACTGT	120
TTGTGCTGGA TCGCAGCGCT GCCTTTCCTT ATG AAG AAG ACA CAA ACT TGG ATT	174
Met Lys Lys Thr Gln Thr Trp Ile	
-25 -20	
CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA	222
Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys	
-15 -10 -5	
ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC	270
Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val	
1 5 10 15	
ACT AAA TTG GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA	318
Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys	
20 25 30	
TAT GTC CCC GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG	366
Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu	
35 40 45	
ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT	414
Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe	
50 55 60	
TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT	462
Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu	
65 70 75	

GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	510
Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	
80 85 90 95	
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT	558
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr	
100 105 110	
CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG	606
Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys	
115 120 125	
GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA	654
Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr	
130 135 140	
TTA AGT CCT GAG AAA GGG AAG GCC AAA AAT CCC CCT GGA GAC TCC AGC	702
Leu Ser Pro Glu Lys Gly Lys Ala Lys Asn Pro Pro Gly Asp Ser Ser	
145 150 155	
CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT CTT ATA ATT	750
Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser Leu Ile Ile	
160 165 170 175	
GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA CAG CCA AGT CTT	798
Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg Gln Pro Ser Leu	
180 185 190	
ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA	846
Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile	
195 200 205	
AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA GAA GTG TAATTGTGGC	895
Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu Val	
210 215 220	
TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA GTTCATGTTT GCTTCATAAA	955
TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA CAGACCACAT CTTTATCTGT	1015
TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG GAACAGAATG TTTTACTGTG	1075
AAACTGGCAC TGA	1088

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:


```

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25                -20                -15                -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
          -5                1                5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
      10                15                20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
      25                30                35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
      40                45                50                55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
          60                65                70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
          75                80                85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
      90                95                100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
      105                110                115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
      120                125                130                135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Gly Lys Ala
          140                145                150

Lys Asn Pro Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu
          155                160                165

Pro Ala Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr
          170                175                180

Trp Lys Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln
      185                190                195

Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
      200                205                210                215

Glu Phe Gln Glu Val
          220

```

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr
1           5           10           15

Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr
          20           25           30

Val Ala Gly Met Asp Val Leu Pro Ser His Xaa Trp Leu Arg Asp
      35           40           45
```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Ile Thr Thr Leu Asn Tyr Val Ala Gly Met
1           5           10
```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Xaa Xaa Leu Gly Pro
1           5           10           15

Glu Lys Asp Ser Arg Val Ser Val Xaa Lys
      20           25
```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Ala Pro Lys Asn Val Glu Ser Leu Lys Lys Pro Thr Arg
1 5 10 15

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asp Arg Ser Ile Asp
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Glu Ser Leu Lys Lys Pro Glu Thr Arg
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Ser Val Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ile	Val	Asp	Asp	Leu	Val	Ala	Ala	Met	Glu	Glu	Asn	Ala	Pro	Lys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	Xaa	Arg
1				5					10			

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val
1				5					10					15	

Ala	Gly	Asp	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg
				20								25

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp
1 5 10 15
Cys Val Leu Ser Xaa Xaa Leu Gly
20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe
1 5 10 15
Phe Ser Ile Phe Xaa Arg
20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe
1 5 10 15
Phe Ser Ile Phe Asp Arg
20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn Ala Pro Lys Asn Val Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Arg Val Ser Val Xaa Lys Pro Phe Met Leu Pro Pro Val Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala
20 25 30

Ser Asp Thr Ser Asp
35

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu
1 5 10 15
Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile
20 25 30
Asp Lys Leu Gly Lys Ile Val Asp
35 40

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Pro Val Ala Ala

1

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCTGAGAAAG ATTCCAGAGTC

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGCAGTTTG TATCTGAAG

19

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CATATAAAGT CATGGGTAG

19

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACTTGTGTCT TCTTCATAAG GAAAGGC

27

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTACGAAAG TAACAGTGTT G

21

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACTGCTCCTA TTTAATCCTC TC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CACTGACTCT GGAATCTTTC TCA

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGACCCGGA TCCCC

15

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCGAGGGGAT CCGGG

15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTTCTTCAT GGCGGCGGCA AGCTT

25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Ser	Arg	Val	Ser	Val	Xaa	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5				10					15		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5					10					15	

Ala Ala

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GGTAC 55

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT 49

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAGGA

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCTCCTGC A

11

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGGAAGGT ATCTGCA

17

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATACCTTCC A

11

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTCCTTATG

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCCGCCGCCA TG

12

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TCTTCTTCAT GGCGGCGGCA AGCTT

25

WHAT IS CLAIMED IS:

1. A non-naturally-occurring polypeptide
having an amino acid sequence sufficiently duplicative
5 of that of naturally-occurring stem cell factor to allow
possession of a hematopoietic biological activity of
naturally occurring stem cell factor.

2. A purified polypeptide comprising
10 naturally-occurring stem cell factor.

3. A polypeptide according to Claim 1 or 2
wherein said polypeptide is the product of procaryotic
or eukaryotic expression of an exogenous DNA sequence.
15

4. A polypeptide according to Claim 3
wherein said polypeptide is the product of CHO cell
expression.

5. A polypeptide according to Claim 3
20 wherein the exogenous DNA sequence is a cDNA sequence.

6. A polypeptide according to Claim 1 or 2
wherein said stem cell factor is human stem cell factor.
25

7. A polypeptide according to Claim 3
wherein the exogenous DNA sequence is a genomic DNA
sequence.

8. A polypeptide according to Claim 3
30 wherein the exogenous DNA sequence is carried on an
autonomously replicating DNA plasmid or viral vector.

35

9. A polypeptide according to Claim 1
possessing part or all of the amino acid sequence of
human stem cell factor as set forth in Figure 15B,
Figure 15C, Figure 42 or Figure 44 or any naturally-
5 occurring allelic variant thereof.

10. A polypeptide according to Claim 1 which
has an in vivo biological activity of naturally-
occurring stem cell factor.

10

11. A polypeptide according to Claim 1 which
has an in vitro biological activity of naturally-
occurring stem cell factor.

15

12. A polypeptide according to Claim 1 or 2
further characterized by being covalently associated
with a detectable label substance.

13. An isolated DNA sequence for use in
20 securing expression in a procaryotic or eukaryotic host
cell of a polypeptide product having an amino acid
sequence sufficiently duplicative of that of naturally-
occurring stem cell factor to allow possession of a
hematopoietic biological activity of naturally occurring
25 stem cell factor, said DNA sequence selected from among:

(a) DNA sequences set out in Figure 14B,
Figure 14C, Figure 15B, Figure 15C, Figure 42,
Figure 44, or their complementary strands;

(b) DNA sequences which hybridize to the DNA
30 sequences defined in (a) or fragments thereof; and

(c) DNA sequences which, but for the
degeneracy of the genetic code, would hybridize to the
DNA sequences defined in (a) and (b).

35

14. A procaryotic or eukaryotic host cell transformed or transfected with a DNA sequence according to Claim 13 in a manner allowing the host cell to express said polypeptide product.

5

15. A polypeptide product of the expression of a DNA sequence of Claim 13 in a procaryotic or eukaryotic host cell.

10

16. An isolated DNA sequence coding for procaryotic or eukaryotic host expression of a polypeptide having an amino acid sequence sufficiently duplicative of that of naturally occurring stem cell factor to allow possession of a hematopoietic biological activity of naturally-occurring stem cell factor.

15

17. A cDNA sequence according to Claim 16.

18. A genomic DNA sequence according to Claim 16.

20

19. A DNA sequence according to Claim 16 wherein said DNA sequence codes for human stem cell factor.

25

20. A DNA sequence according to Claim 19 and including one or more codons preferred for expression in E. coli cells.

30

21. A DNA sequence according to Claim 16 having the sequence set out in Figure 15B, Figure 15C, Figure 42 or Figure 44.

22. A DNA sequence according to Claim 16 and including one or more codons preferred for expression in yeast cells.

35

23. A DNA sequence according to Claim 16 covalently associated with a detectable label substance.

24. A DNA sequence coding for a polypeptide
5 fragment or polypeptide analog of naturally-occurring stem cell factor.

25. A DNA sequence as in Claim 24 coding for methionyl stem cell factor.
10

26. A biologically functional plasmid or viral DNA vector including a DNA sequence according to Claim 16.

27. A procaryotic or eukaryotic host cell stably transformed or transfected with a DNA vector according to Claim 26.
15

28. A polypeptide product of the expression
20 in a procaryotic or eukaryotic host cell of a DNA sequence according to Claim 16.

29. A polypeptide having part or all of the amino acid sequence as set forth in Figure 15C,
25 Figure 42 or Figure 44 and having one or more of the in vitro biological activities of naturally-occurring stem cell factor.

30. A polypeptide having part or all of the secondary conformation of naturally-occurring stem cell factor and having part or all of the amino acid sequence set forth in Figure 15C, Figure 42, or Figure 44 and having a biological property of naturally-occurring human stem cell factor.
35

31. A process for the production of stem cell factor comprising:

growing, under suitable nutrient conditions, procaryotic or eukaryotic host cells transformed or
5 transfected with a DNA according to Claim 13, and isolating desired polypeptide products of the expression of DNA sequences in said vector.

32. A composition comprising a purified and
10 isolated human stem cell factor free of association with any human protein in glycosylated or nonglycosylated form.

33. A pharmaceutical composition comprising
15 an effective amount of a polypeptide according to Claim 1 and a pharmaceutically-acceptable diluent, adjuvant or carrier.

34. A method for treatment of leucopenia in a
20 mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

35. A method for treatment of
25 thrombocytopenia in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

30 36. A method for treating anemia in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

35 37. A method for enhancing engraftment of bone marrow during transplantation in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

38. A method of enhancing bone marrow recovery in treatment of radiation, chemical, or chemotherapeutic induced bone marrow aplasia or myelosuppression which comprises treating patients with therapeutically effective doses of stem cell factor.

39. A DNA sequence coding for an analog of human stem cell factor selected from the group consisting of:

- a) [Met⁻¹] stem cell factor; and
- b) stem cell factor wherein one or more cysteines are replaced by alanine or serine.

40. A polypeptide product of the expression in a procaryotic or eukaryotic host cell of a DNA sequence according to Claim 39.

41. A pharmaceutical composition comprising recombinant stem cell factor having the human amino acid sequence, and a pharmaceutically acceptable diluent, adjuvant or carrier.

42. An antibody specifically binding stem cell factor.

43. An antibody as in Claim 42 wherein said antibody is a monoclonal antibody.

44. A process for the efficient recovery of stem cell factor from SCF containing material, the method comprising the step of subjecting the SCF containing material to ion exchange chromatographic separation.

45. A process as in Claim 44 wherein said ion exchange chromatographic separation is anion exchange chromatographic separation.

5 46. A process as in Claim 44 further comprising the step of reverse phase liquid chromatographic separation.

10 47. A process for the efficient recovery of stem cell factor from SCF containing material, the method comprising the step of subjecting the SCF containing material to reverse phase liquid chromatographic separation.

15 48. A polypeptide having the hematopoietic biological activity of naturally occurring stem cell factor, said polypeptide having an amino acid sequence set forth in Figure 15C, Figure 42 or Figure 44 or any allelic variants, derivatives, deletion analogs,
20 substitution analogs, or addition analogs thereof, and characterized by being the product of procaryotic or eucaryotic expression of an exogenous DNA sequence.

25 49. A polypeptide as in Claim 48 selected from the group consisting of:
 SCF²-164, SCF⁵-164, SCF¹-130,
 SCF¹-148, SCF¹-162, SCF¹-164, SCF¹-165, SCF¹-183
 (Figure 15C); SCF¹-185, SCF¹-188, SCF¹-189, and SCF¹-248
 (Figure 42); and SCF¹-157, SCF¹-160, SCF¹-161 and
30 SCF¹-220 (Figure 44).

 50. A biologically active composition comprising the polypeptide of Claim 1 covalently attached to a water-soluble polymer.

51. A composition as in Claim 50 wherein said polymer is selected from the group consisting of polyethylene glycol or copolymers of polyethylene glycol and polypropylene glycol, and said polymer is
5 unsubstituted or substituted at one end with an alkyl group.

52. The composition of Claim 50 wherein the polypeptide is [Met⁻¹] SCF¹-164.
10

53. The composition of Claim 50 wherein said polymer has an average molecular weight of about 1,000 to 100,000 daltons.

54. The composition of Claim 50 wherein said polymer has an average molecular weight of about 4,000 to 40,000 daltons.
15

55. The composition of Claim 50 wherein said polymer is an unsubstituted polyethylene glycol or a monomethoxy polyethylene glycol.
20

56. The composition of Claim 50 wherein said polymer is attached to said polypeptide via reaction
25 with an active ester of a carboxylic acid or carbonate derivative of said polymer.

57. The composition of Claim 50 wherein one or more amino groups of said protein are conjugated to
30 said polymer by reaction with a N-hydroxysuccinimide, p-nitrophenol or 1-hydroxy-2-nitro-benzene-4-sulfonate ester of the polymer.

58. The composition of Claim 50 wherein one
35 or more free cysteine sulfhydryl groups are conjugated to said polymer via reaction with a maleimido or haloacetyl derivative of the polymer.

59. The composition of Claim 50 wherein the polypeptide is glycosylated and the polymer is attached by reaction of an amino, hydrazine or hydrazide derivative of the polymer with one or more aldehyde groups generated by oxidation of the carbohydrate moieties.

60. A method for preparing a biologically active polymer-polypeptide adduct which comprises reacting the polypeptide of Claim 50 with a water-soluble polymer under conditions permitting the covalent attachment of the polymer to said polypeptide, and recovering the adduct so produced.

61. A method of treating acquired immune deficiency in a human comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

62. A method of treating neoplasia in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

63. A method as in Claim 62 wherein before said administering step is the step of administering chemotherapy or irradiation to said mammal.

64. A method of transfecting early hematopoietic progenitor cells with a gene comprising:
(i) culturing early hematopoietic progenitor cells with SCF; and
(ii) transfecting the cultured cells of step (i) with a gene.

65. A method of transferring a gene to a mammal comprising the steps of:

(i) culturing early hematopoietic progenitor cells with SCF;

5 (ii) transfecting the cultured cells of step (i) with a gene; and

(iii) administering the transfected cells to said mammal.

10 66. A method of treating nerve damage in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

15 67. A method of treating infertility in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

20 68. A method of treating intestinal damage in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1.

25 69. A method of treating myeloproliferative disorder in a mammal comprising administering a therapeutically effective amount of the polypeptide according to Claim 1 conjugated to a toxin.

30 70. A polypeptide as in Claim 48 selected from the group consisting of:

[Met⁻¹]SCF¹-148, [Met⁻¹]SCF¹-162,
[Met⁻¹]SCF¹-164, [Met⁻¹]SCF¹-165, [Met⁻¹]SCF¹-183
(Figure 15C); [Met⁻¹]SCF¹-185, [Met⁻¹]SCF¹-188,
35 [Met⁻¹]SCF¹-189, and [Met⁻¹]SCF¹-248 (Figure 42); and
[Met⁻¹]SCF¹-157, [Met⁻¹]SCF¹-160, [Met⁻¹]SCF¹-161 and
[Met⁻¹]SCF¹-220 (Figure 44).

STEM CELL FACTOR

ABSTRACT OF THE DISCLOSURE

5 Novel stem cell factors, oligonucleotides
encoding the same, and methods of production, are
disclosed. Pharmaceutical compositions and methods of
treating disorders involving blood cells are also
disclosed.

10

15

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25

30

A-175-CIP4

35

FIG.1

HPP-CFC (Colony #)

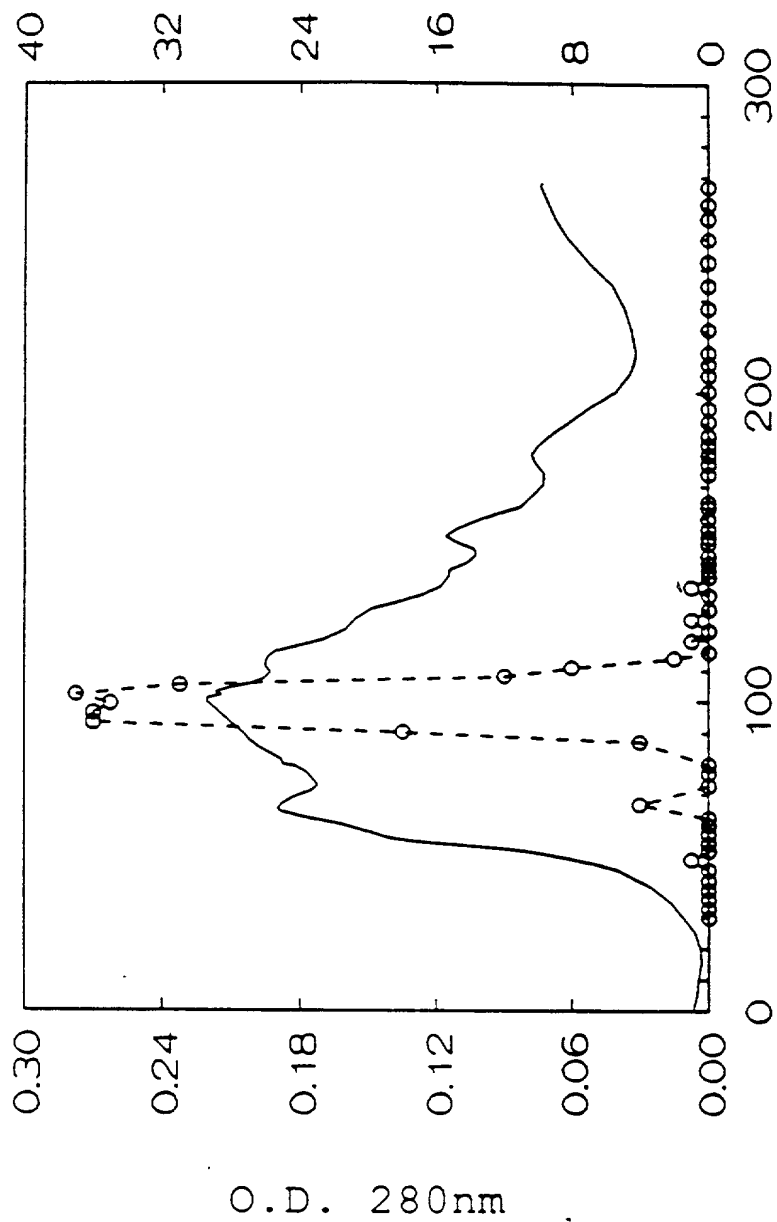
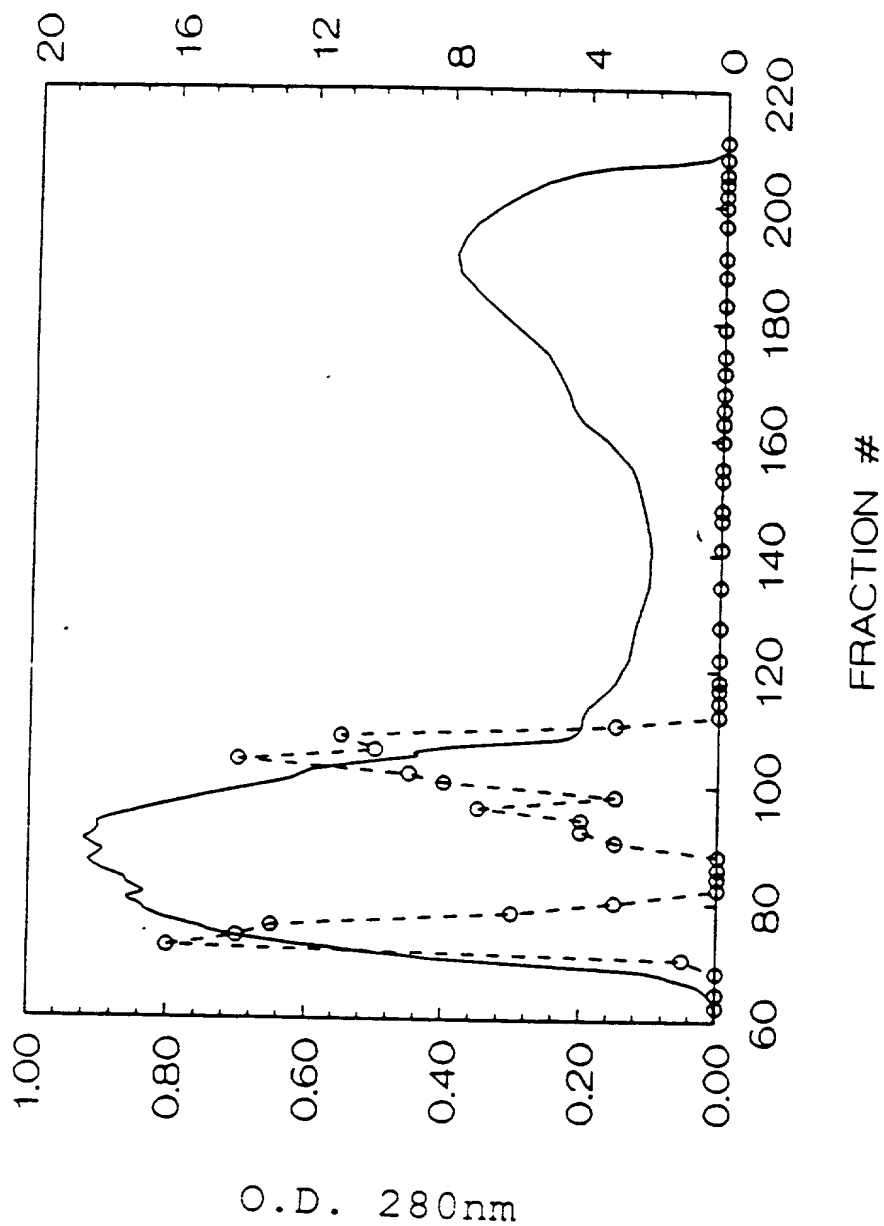


FIG.2

HPP-CFC (Colony #)



— O.D. -○- HPP-CFC

FIG.3

MC/9 CPM (X 10⁻³) OR HPP-CFC (col. #)

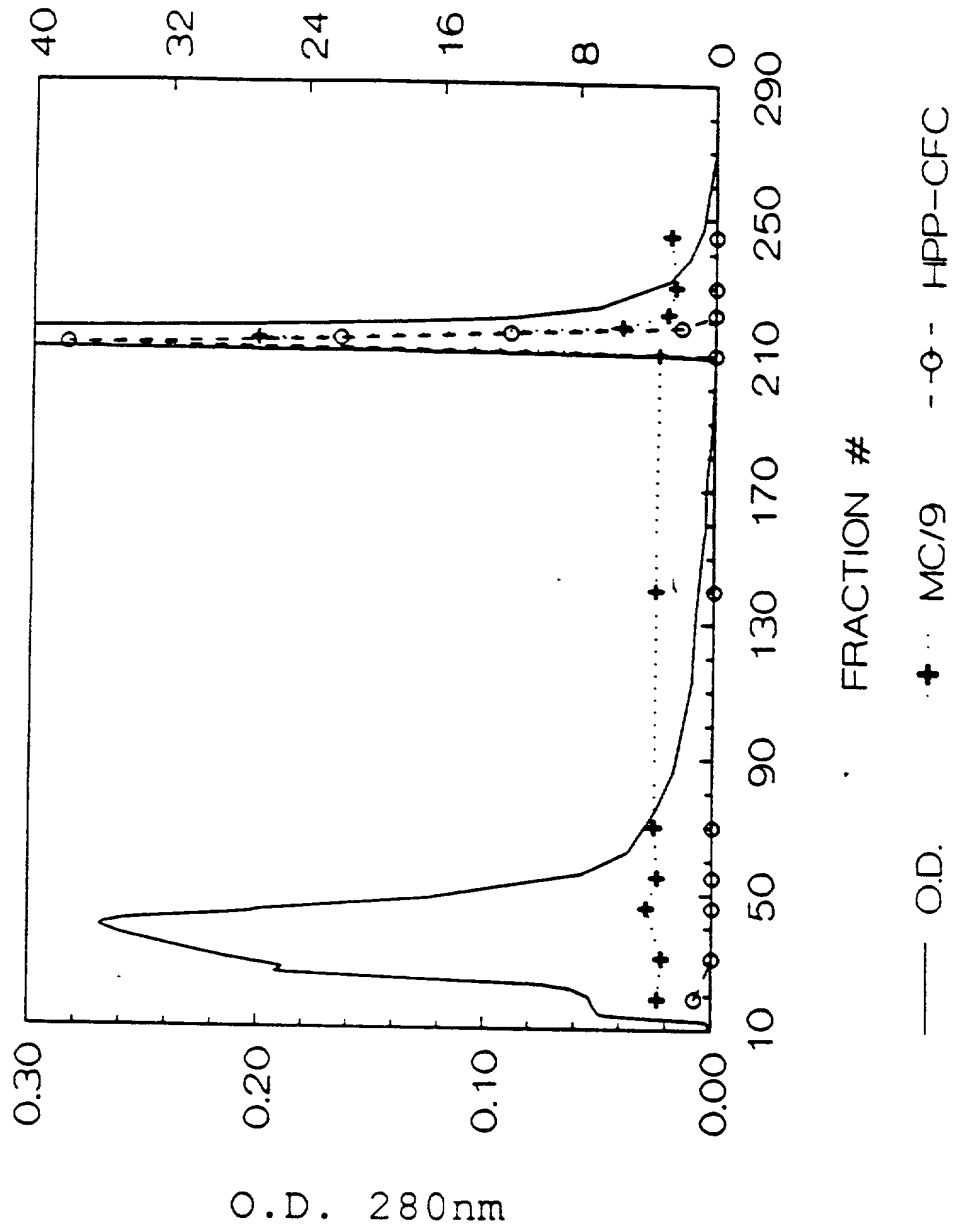
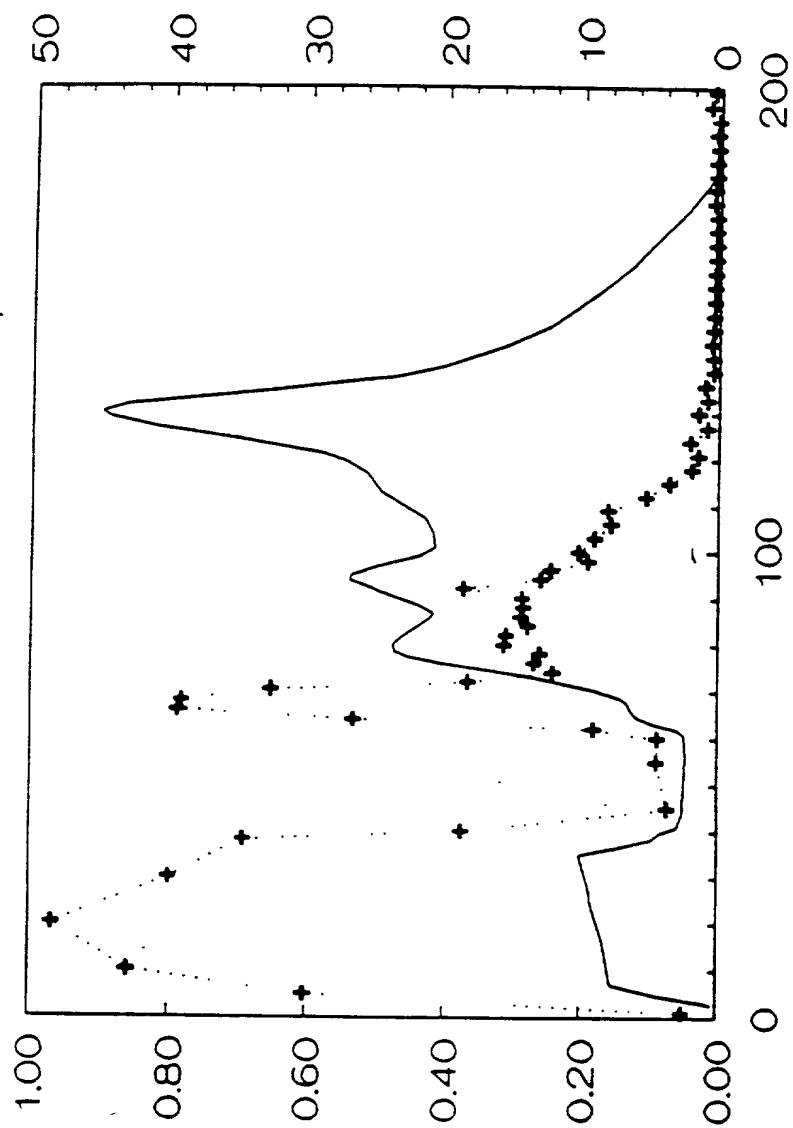


FIG. 4

MC/9 CPM ($\times 10^{-3}$)



FRACTION #

— O.D.

···+ MC/9

O.D. 280nm ($\times 10^1$)

FIG.5

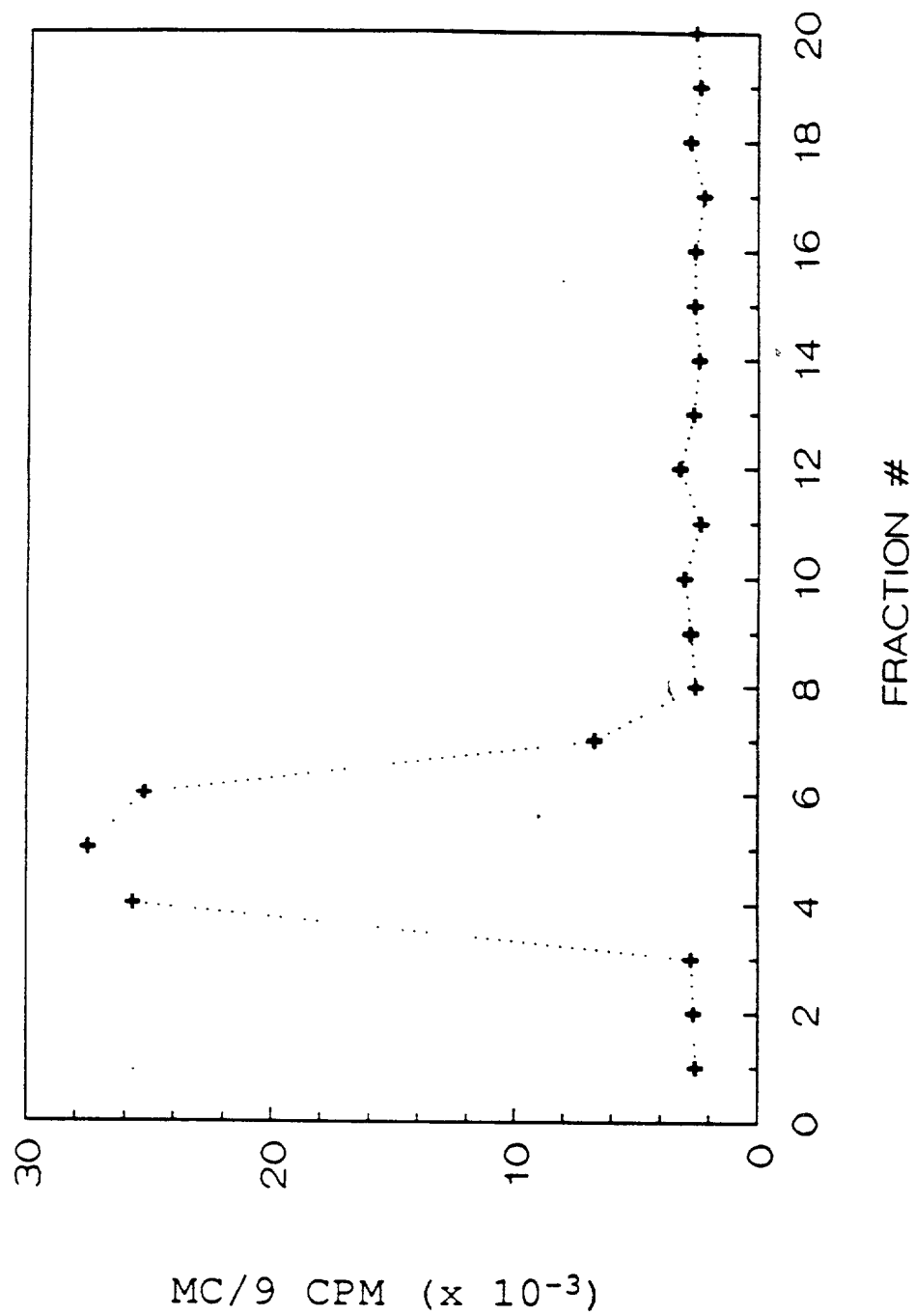


FIG. 6

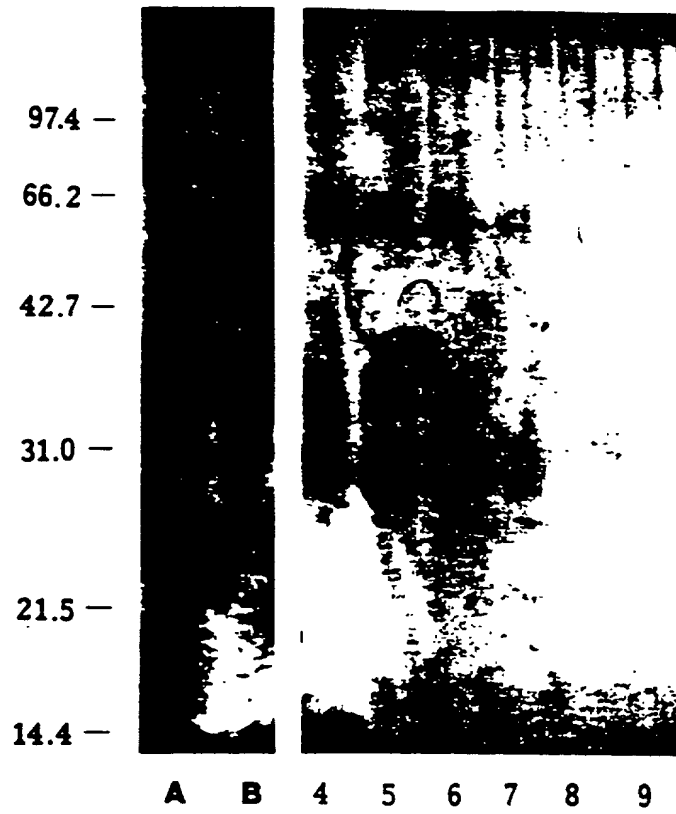
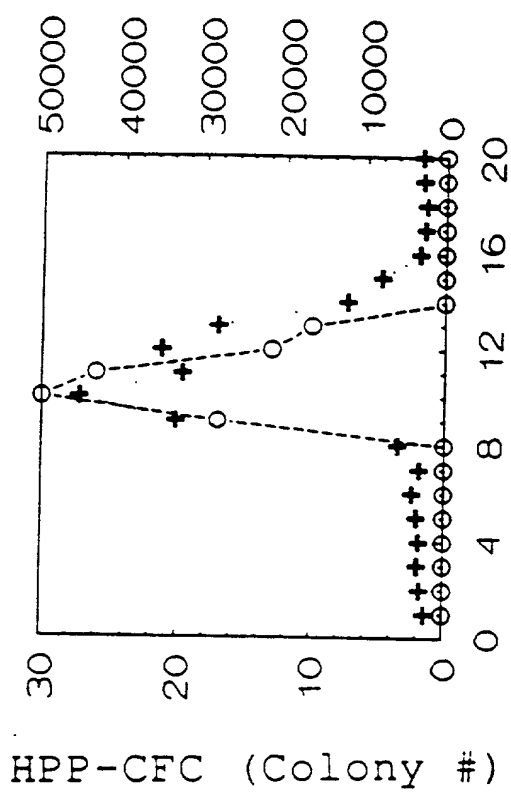


FIG.7

MC/9 CPM



FRACTION #

--o-- HPP-CF ...+ MC/9

FIG. 8

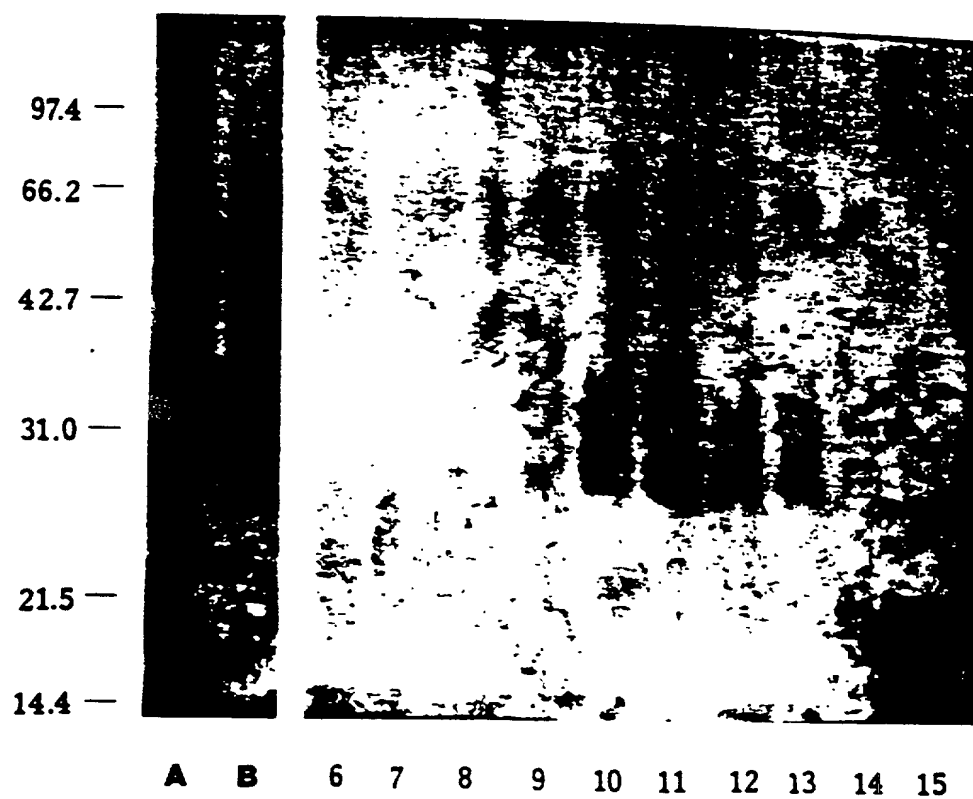


FIG.9

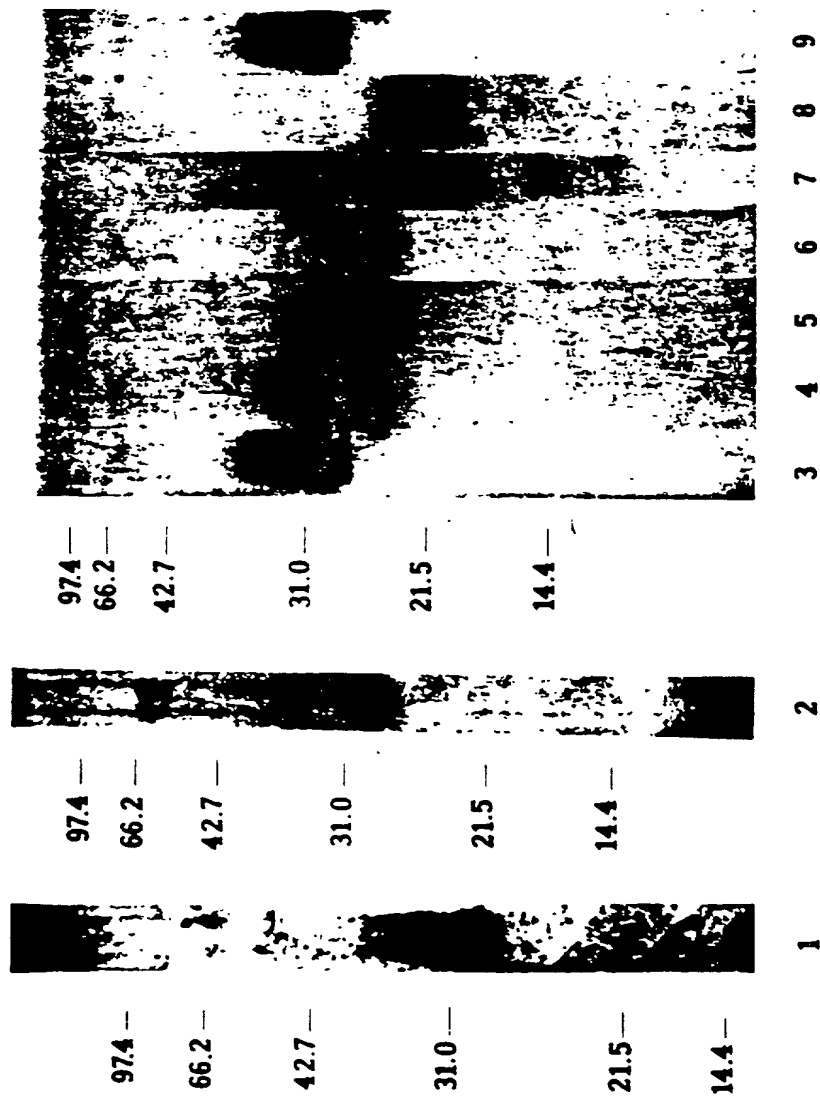
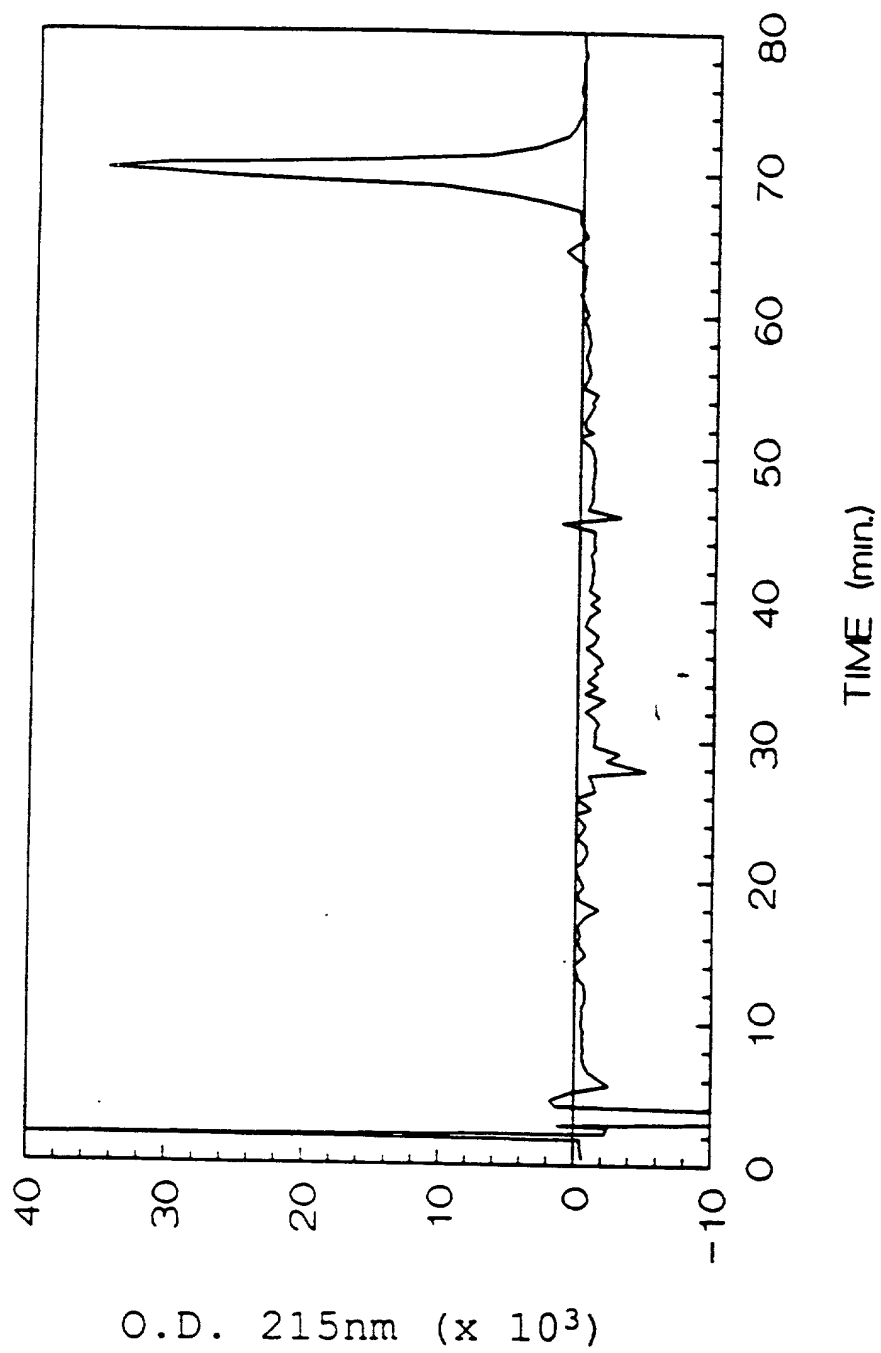


FIG.10



	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

```

1      10      20
pE E I C R N P V T D N V K D I T K L V A N L P N D
----- Sequencing after -----
                        T-5a -----
30      40      50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment ----->
----- T-5a -----
----- CB-6a ----- CB-8; CB-10 -----
60      70
H L S V S L T T L L D K F S N I S E G L S N Y S I
----- Sequencing after Trp Cleavage -----
80      90      100
I D K L G K I V D D L V A C M E E N A P K N V K E
----->
----- T-3 -----
----- CB-14; CB-15; CB-16 -----
                        S-1 -----
110     120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 ----- T-4 (N109 nonglyco) -----
----- T-7 (N120 glyco); T-8 (N109 nonglyco) -----
----- CB-14; CB-15; CB-16 -----
----- S-5 or S-6 (N109 nonglyco) -----
130     140     150
F K D F M V A S D T S D C V L S S T L G P E K D S
----- T-5b -----
----- CB-6B -----
----- S-5 or S-6 -----
160
R V S V T K P F M L P P V A(A)
----- T-2 -----
----- CB-6B -----
----- S-2 -----

```

FIG.12A

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTIGGIGCATTTCTCCTCCAT G T G T T	393-368
219-22	AAAAACTCCTCIGGIGTAAATTT G T T G G	447-425
219-25	GTTTCNGGTTTTTT C C C	420-407
219-26	ATGGAAGAAAACGCCCCCAAAACGT G G T G T	368-393
222-11	CCNAATGATTATATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTTAAAI CGATC G G C G G	492-470
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG.12A cont.'

224-28	TAACCAACAATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTG	547-562
227-29	GCGAAGCTTGCCCTTTCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCGCGGAACCTTAAGTCCATGCAACAC	705-685 *
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595 *

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCCTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190 *

FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

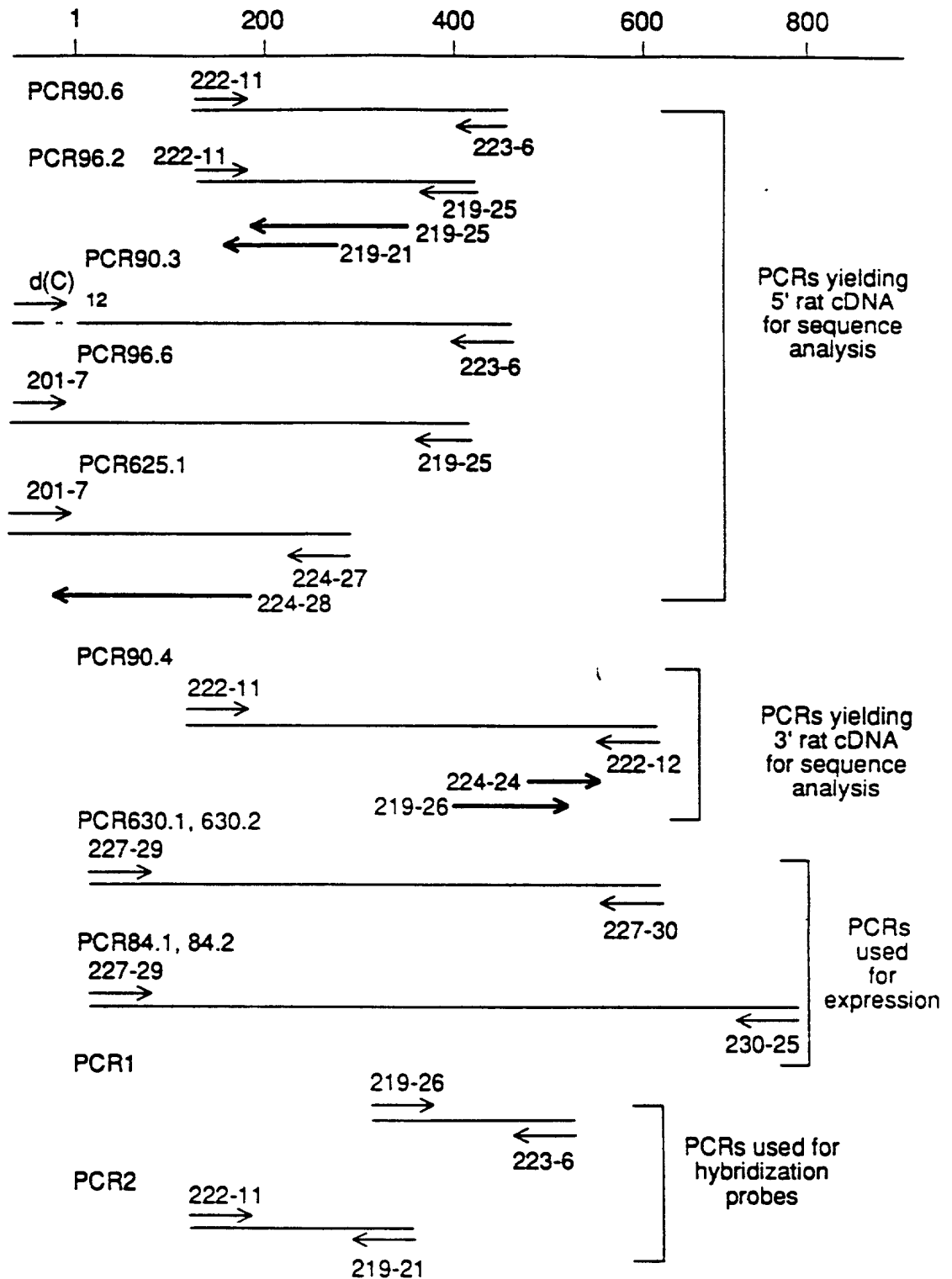


FIG.13B

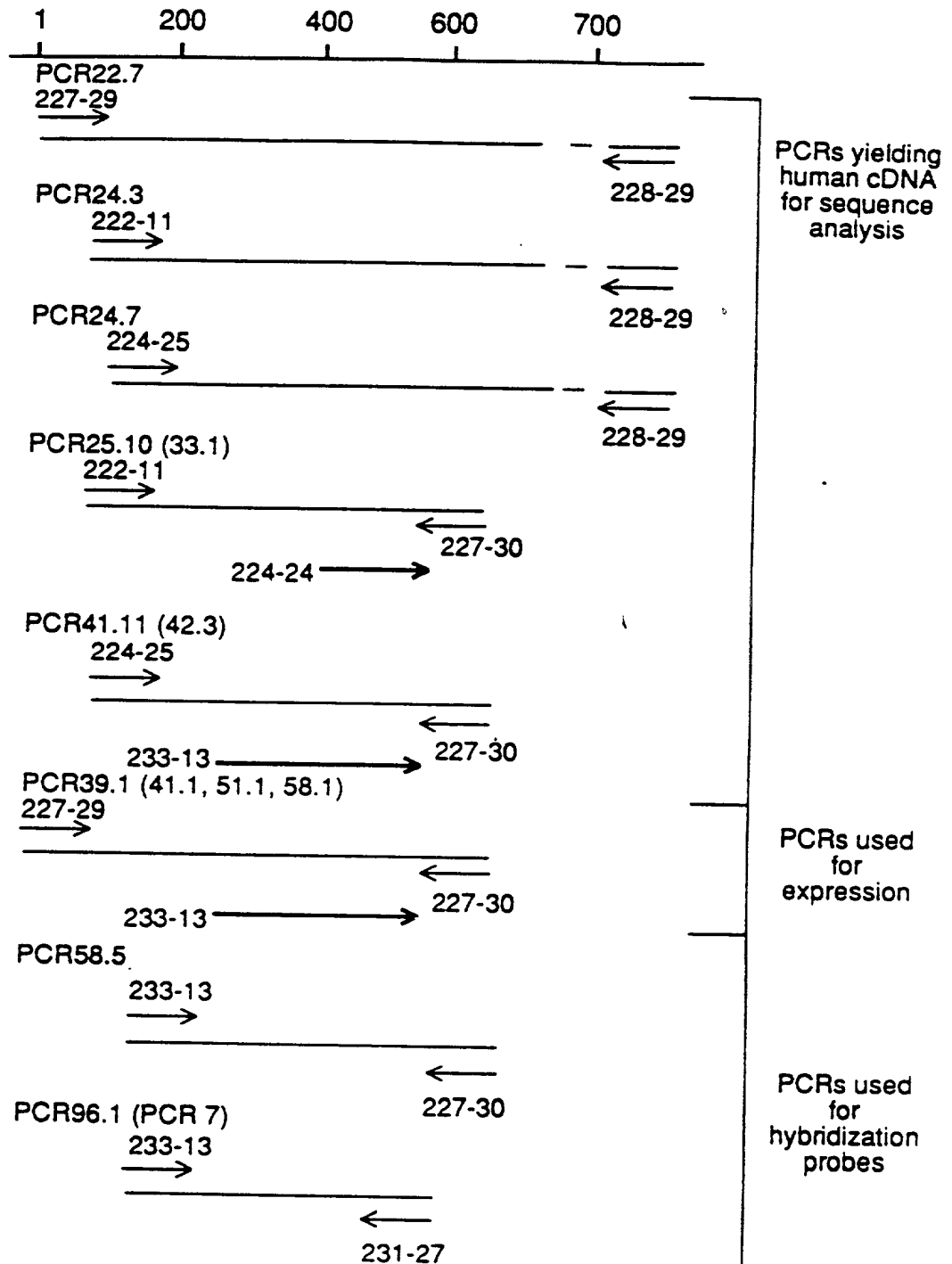


FIG. 14A

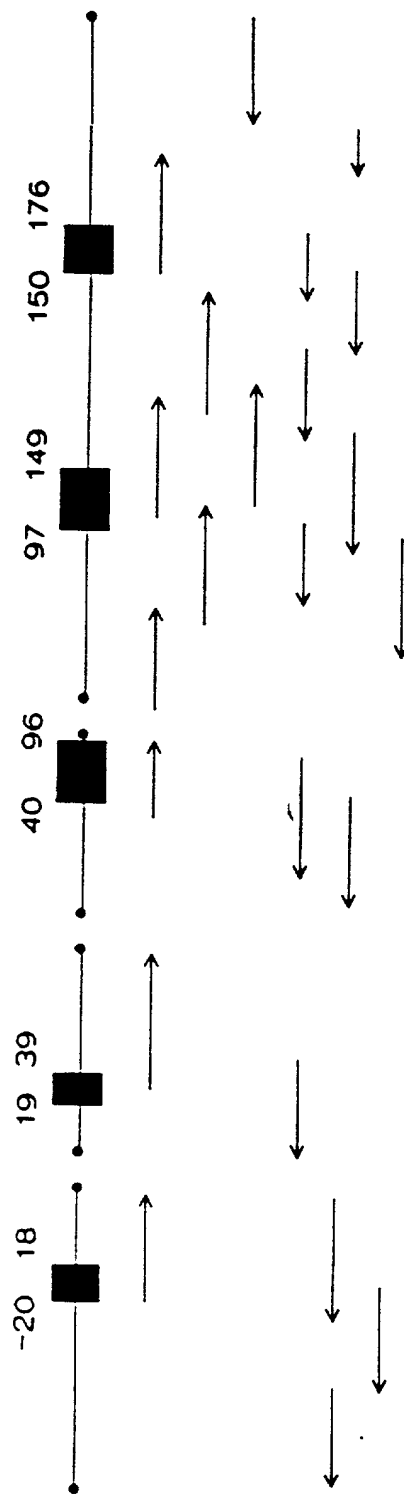


FIG.14B

AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT	45
AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT	90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA	135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT	180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG	225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTCATGCATTCCT	270
CCATTTTCCGAGGTCCCccCcAAGTGATAATTCTGTTACACGTTG	315
CTACAAGTTCATCCCTAATTGCCGTCAAGAACTGACTGTAGAAG	360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT	405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC	450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT	495
AAGCCATCAGCTTAAAACAAAACAAAACAAAAAAAACCC	540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC	585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTTAAAACTGATGGAC	630
	-20
	ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT	675
	-10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG	
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAACTC	720
	1 10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT	
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA	765
	18
hrLysLeu	

FIG.14B CONT.'

CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC	810
CTGTGCTTGCTGACCACATAGGTTTCAGGGCACTCCCGACAGGAGT	855
TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC	900
TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC	945
TGTATAACTGGCCCTTTGCACACCAACAAAGTGAAGTGAAGTGC	990
TTGCCTGTTACCTACTG	1007

Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA	45
TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA	90
TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT	135
	19
	Val
TCTCTTGTATTTACTCACGTTTTTCATTTCTTGGTCTCTGTAGGTG	180
	30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla	
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC	225
	39
GlyMetAspValLeu	
GGGATGGATGTTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT	270
TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT	315
TATTTGCTCTTTGTCGTTTTTTAGATGTTGACCTATAATTTTTCCT	360
TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT	405
TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA	450

FIG.14B CONT.'

CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG	495
TTAAAATCATGTAAATTTTCCTCCTTGGCTATGTTATTTCTCATG	540
GCTATGTTATTCCTATTCGTATTTTCATTTAAAGGGACGGAATATT	585
TATTGTATTTCTGAACTTTTTTCAGGCATGCATCCGGGTCTTTGAA	630
TAAAA	635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA	45
ATGTCTTTGAAAACGCAGTGAATAAGCCATAAATAATCTTCCACA	90
GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG	135
AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG	180
GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT	225
TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT	270
TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAACTCTTTGTCTCT	315
GCAGTCAGTGAATAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA	360
ATCTGCCATATTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTTC	405

40

50

ProSerHisCysTrpLeuArgAspMetValThrHisLeu	
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA	450

60

SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer	
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT	495

70

80

GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle	
---	--

FIG.14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90

96

ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585

ACTTGGTATTCATCAGAATTATTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90

ATATGTAGATAACCACCTCTGCCACCTCAGCACATACATACACATA 135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225

TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT 270

AATTGTTTTTTTCGGGTCACTTTATTGTCCTATTGCCACGACATTG 315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT 450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495

AGTCAAGTCTATGAGTTATTTGAAAAC TAGAATCTTTGTTAATTA 540

97

AsnValLys

TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100

110

GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAACTAGAACTTTACTCCTGAAGAA	630
120	
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC	675
130	140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA	720
148	
GlyProGluLysA GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT	765
ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC	810
TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA	855
ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT	900
GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA	945
AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT	990
GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA	1035
AGATTTACAGTCTCATGTCTTTTCCATAAGGTTCAAACCTCTGAGA	1080
CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC	1125
CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT	1170
AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT	1215
TCCTAAGCATGTCTGTGCATGCATAAGCCTTCACTCTACAAGAC	1260
AGTTATGGTGTATCGCTTGACAAAACCTGAGCAGCCAAGCTGAGTA	1305
TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT	1350
GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAGTTCA	1395

FIG.14B CONT.

	150	
	spSerArgV	
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG		1440
	160	
alSerValThrLysProPheMetLeuProProValAlaAlaSerS		
TCAGTGTCAAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT		1485
	170	176
erLeuArgAsnAspSerSerSerSerAsn_		
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC		1530
TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT		1575
GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG		1620
TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG		1665
TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA		1710
ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC		1755
GAAATTAATTGAAGGAAAAAAAAATAACAAGCAAGGCCTTATTTTG		1800
AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT		1845
CAAAGTGGAGTTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC		1890
AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG		1935
CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA		1980
TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT		2025
TGcCCAAGAACCCAcGTTcCTGGAAGACTATCTTATTTTCATGTC		2070
TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT		2115
CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA		2160
AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA		2205

CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC

FIG.14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC	2250
CCTGAAAAATATATTTTACAGTGTAGACATTTGATATACATCTAA	2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC	2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC	2385
ATGCATATAACATATCAGATCCTCGAGC	2413

FIG.14C

-25 -20
 M K K T Q T W I I T C I
 CTGGATCGCAGCGCTGCCTTTCCTTATGAAGAAGACACAACTTGGATTATCACTTGCAT 60

 -10 1
 Y L Q L L L F N P L V K T Q E I C R N P
 TTATCTTCAACTGCTCCTATTAACTCCTCGTCAAAACTCAGGAGATCTGCAGGAATCC 120

 10 20
 V T D N V K D I T K L V A N L P N D Y M
 TGTGACTGATAATGTAAAGACATTACAAACTGGTGGCGAATCTTCCAAATGACTATAT 180

 30 40
 I T L N Y V A G M D V L P S H C W L R D
 GATAACCCCTCAACTATGTCCGGGATGGATGTTTGGCCTAGTCATGTTGGTTACGAGA 240

 50 60
 M V T H L S V S L T T L L D K F S N I S
 TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTC 300

 70 80
 E G L S N Y S I I D K L G K I V D D L V
 TGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAATAGTGGATGACCTCGT 360

 90 100
 A C M E E N A P K N V K E S L K K P E T
 GGCATGTATGGAAGAAAATGCACCTAAGAATGTAAAGAATCACTGAAGAAGCCAGAAAC 420

 110 120
 R N F T P E E F F S I F N R S I D A F K
 TAGAAAACCTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTCATGATGCCTTCAA 480

FIG. 14C cont.

130		140	
D F M V A S D T S D C V L S S T L G P E			540
GGACTTCATGGTGGCATCTGACACTAGTGTGCTCTCTTCAACATTAGGTCCTGA			
150		160	
K D S R V S V T K P F M L P P V A A S S			600
GAAAGATCCAGAGTCAGTGTCACAAAACCATTATGTTACCCCTGTTGCAGCCAGTTC			
170		180	
L R N D S S S S N R K A A K S P E D P G			660
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAGCCGCAAGTCCCCTGAAGACCCAGG			
190		200	
L Q W T A M A L P A L I S L V I G F A F			720
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTTCGCTTGTAAATGGCTTTGCTTT			
210		220	
G A L Y W K K K Q S S L T R A V E N I Q			780
TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAAATATACA			
230		240	
I N E E D N E I S M L Q Q K E R E F Q E			840
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTCAGA			
248			
V			849
GGTGTAAAT			

FIG.15A

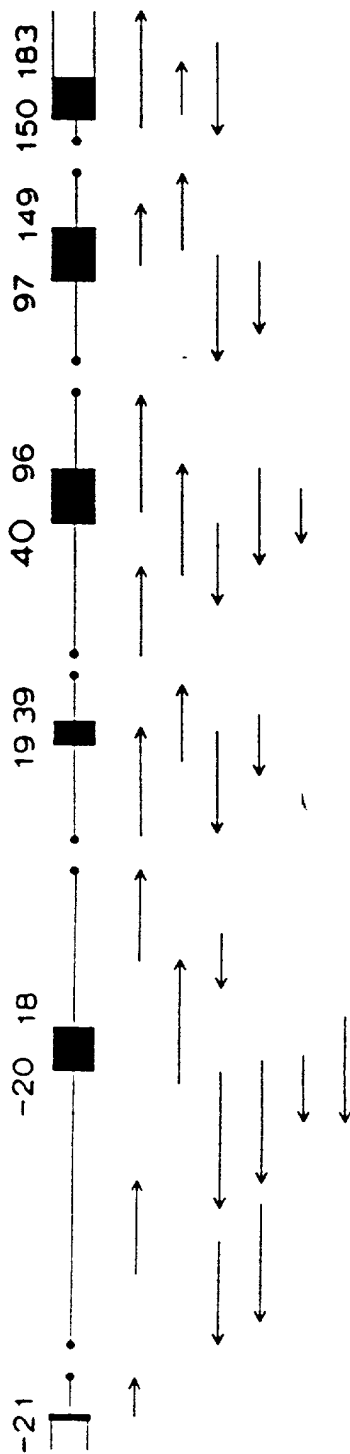


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA	45
AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT	90
TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG	126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA	45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT	90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG	135
TGTTGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG	225
GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT	270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT	315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA	405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT	450
CTCTAGTTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC	495
TGCTACAAGTTTATTCTTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTAAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT	585
CAAAATGGATTTTAACTAAAAGCTTTTAAAACTTTGGTGAGCAT	630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT	675

FIG.15B CONT.'

ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT	720
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC	765
<div style="display: flex; justify-content: space-between; width: 100%;"> -20 -10 </div> <div style="display: flex; justify-content: space-between; width: 100%;"> ThrTrpIleLeuThrCysIleTyrLeuGlnLe </div> TGTTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT	810
<div style="display: flex; justify-content: space-between; width: 100%;"> 1 </div> uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs GCTCCTATTTAATCCTCTCGTCAAACTGAAGGGATCTGCAGGAA	855
<div style="display: flex; justify-content: space-between; width: 100%;"> 10 18 </div> nArgValThrAsnAsnValLysAspValThrLysLeu TCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA	900
GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT	945
CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT	990
AATGTTTTCTCTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA	1035
GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080
TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT	1125
TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT	1170
TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC	1215
CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA	1260
CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT	1305
GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC	1350
ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT	1395
CATTGCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT	1440
TGAACTCTTCCCTCAGCGAAAGCATTGTCATTGCTTCCC	1479

FIG.15B CONT.'

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC	45
CAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA	90
GTCTAAAAGATCTGTATTATCACTTTTTTATTTTGAAGGATGCCT	135
TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT	180
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAAACAGTTTTG	225
TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA	270
	19
	ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTTGTCTCTGTAGGTGGCAA	315
	30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA	360
	39
etAspValLeu	
TGGATGTTTTGGTATGTAACTACATTTCTGAGTTTCATTTTAGT	405
AGCTCATAGAAGAAATGGGATCATTATATTGAGATAGTACACTA	450
GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA	495
TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT	535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT	45
CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC	90

FIG.15B CONT.'

CTCCTATTACAACATTTTAAAGTAATGTAATATTAATTTTAAAAAT	135
CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG	180
AAGCTGAGACGGGTGGATCATTGAGGTCAGGAAGTTTGAGACAG	225
CCTGGCCAACATGGTGAACTTCCTCTCTACTAAAAATAAAAAAG	270
TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA	315
GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG	360
AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT	405
40	
ProSerHisCysTrpIleS	
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA	450
50 60	
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA	
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG	495
70	
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA	540
80 90	
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL	
TAGACAAACTTGTTGAATATAGTGGATGACCTTGTGGAGTGCCTGA	585
96	
ysGluAsnSerSerLys	
AAGAAAACATCATCTAAGGTAACCTTGTGTTCATTGGGATTATTTT	630
TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG	675
AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC	720
AAATTTAAAAATCTTGTTTCAGATGAGCAAAGAAAACAAGTATTTG	765
CAGTTATACTGCAATACTGAAGTGCACATTC	796

23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIG.15B CONT.'

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA	45
CTACCCTGCATTACCAATCTGAATTACATACGTTAAAACAGCCAT	90
CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA	135
GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180
	97
	AspLeuLysL
CTATTTGAAAAATGTAATCCTATTTTTTTCTTCTAGGATCTAAAAA	225
	110
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP	
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT	270
	120
	130
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV	
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG	315
	140
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS	
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA	360
	148
erProGluLysA	
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCAGTTCAAATGTA	405
AACAACAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG	450
TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG	495
CAGATATCAATAGCACAGAAGAAA	519

Intervening sequence of unknown length

FIG.15B CONT.'

CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG	45
150	160
spSerArgValSerValThrLysProPheMetL	
CTTTCTATTTAGATTCCAGAGTCAGTGTACAAAACCATTTATGT	90
170	
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS	
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA	135
176	
erAsnA	
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA	180
ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCT	225
ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA	270
TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG	315
CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT	352

FIG. 15C

-25

-20

M K K T Q T W I L T C I Y L Q
AAGCTTGCCTTTCCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCATTATCTTCAG 61

-10-

1

[illegible]

20

30

N V K D V T K L V A N L P K D Y M I T L
AATGTAAGAAGCGTCACTAAATTGGTGGCAATCTTCCAAAAGACTACATGATAACCCCTC

40

50

K Y V P G M D V L P S H C W I S E M V V
AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTA 241

60

70

Q L S D S L T D L L D K F S N I S E G L
CAATTGTCAGACAGCTTGACTGATCTCTGGACAAGTTTCAAATATTTCTGAAGGCTTG 301

80

90

S N Y S I I D K L V N I V D D L V E C V
AGTAATTATTCATCATAGACAAACTGTGTAATATAGTGGATGACCTTGTGGAGTGGCGTG

100

110

K E N S S K D L K K S F K S P E P R L F
AAAGAAAACATCATAGGATCTAAAAAATCATTCAGAGCCAGAACCCAGGCTCTTT 421

FIG.15C cont.'

T P E E F F R I F N R S I D A F K D F V	120	130
ACTCCTGAAGAATTCTTTAGAAATTTTAAATAGATCCATTGATGCCTTCAAGGACTTTGTA		481
V A S E T S D C V V S S T L S P E K D S	140	150
GTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAAAGTCCTGAGAAAGATTCC		541
R V S V T K P F M L P P V A A S S L R N	160	170
AGAGTCAGTGTCACAAACCATTTATGTACCCCTGTGTCAGCCAGCTCCCTTAGGAAT		601
D S S S S N S K Y I Y L I	180	183
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGGCTCCAAT		661
TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTGA		721
TACTGTTCTGTACTGTTATTCCCTTTTATGGTCTTCTTGAGACTTAAAGTTTGTAGAATTA		781
AATTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG		820

FIG. 15D

GAGCTCCGAGCCcTcTcTGGCGcGcGAGGTATTTCGTCTGTnCCCCGGGGTGCCAGGTGA 60
 GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120
 AAGCTTCGCCCTCTGCGTCCCCCGGCCCTTCGGGGTCTCCCGCCAGTGCAGGTCCGGGGCC 180
 CCCAGCGAGCGGACAAAGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC 240
 TGGCCGCCCTCCCGATTCTTCCCTCCGGCCCTTGCCCTGCTTCTCGCCTACCCCGGGCTC 300
 CGGAAGGGAAGGAGGCGTGTCCGGAGCAGCGGGCGGGAACGTATATAAAGCGCCGGCGG 360
 CTCAGCAGCCGGCTTCGCTCGCCGCCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGG 420
 GACAGTGGAGAGGGCGCTGGGCTCGGGCTACCCAATGCGTGGACTATCTGCCGCCCGCTGT 480
 TCGTGCAATCTTGTGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC 540

-25 -21
 MetLysLysThrGln

TGGATCGCAATCTGTGCCCTTTCCTTATGAAGAAGACACAAGTGAGTAGGGCGGCCGGGA 600
 GCTCCCAGGCTCTCCAGGAAAAATCGGCCCGGCTGCCCGGGGAAGCCGGCTCCCTGG 660
 GACTTGCAGCTGGGGCGTGCAGGGCTGTGCCCTGCCGGGTGAGACAAGAGGATGCGGGGGA 720
 GGCCGGCGTGGTGTGATCCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAGGAGTGGGA 780
 GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTGGAGCTGTCAG 840
 TCGGAAACCGTAATTCCTCGTCTGGTGGAAAGATTGGCTTTTnGnCCACGGAATGTAAGTT 900
 ATCAC

FIG. 15D CONT.

Intervening sequence of unknown length

AGATACTACAAAGATAAAATCAGTTGCACAAGTCTTGAAACTCTACAGTGTAAATAAGGAA	60
AAATAAGTCATGCATAAAAAGCAACTATAATAACATAATAGAAAAATGTTATTTTCAAGCCGA	120
TGTGTAGGTTATGTGTGTTTCGAGAGAGAGAGAGAGAACAGACAGATTACTTTCTGTCTAGGGT	180
TCAAGAAATGCCCTTCCTGGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAAAAAGCTGTGT	240
TTCAAAAATATTCCTTTTGATGTCTCACAAATTCAGTGGAAATCTCTTAGGCTCAAAAAATAT	300
ACATCTCTCTCACCTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACCTGCTCA	360
GGGATTATGCTGCTTCTTGCCCAAGCAGCTACATTTAAAGTAGAAAAATAAGATGTTTCTTT	420
TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCCTAAGGGCT	480
AAGTCTTTAACAATGCTGCTACAAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTTAACAATAAGTTAAACAATATTGTTCATTGAGAGAATAATTCAAAAATGGATTTTAA	600
CTAAAAGCTTTTAAAAAAGCTTTGGTGAGCATAGCTTGAATGCCGTAATATTAAATTGCATTT	660
AAGCCAATAACATATATTAGACTGGTCTTTTTTGTGCATCAAGGCATTAGATGTTAAAAAGT	720
-20	
TTGAATGATTACAGATCTTAAGTATGATGATCACCACCAAGCAATTTTCTGTTTTCATTTAGAC	780
Th	
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuPheAsnProLeuValLysThrG1	
TTGGATTCTCAGTTCGATTTTATCTTCAGCTGCTCCTATTAAATCCCTCTCGTCAAAACTGA	840

FIG. 15D CONT.

1	10	18
uGlyIleCysArgAsnArgValThrAsnAsnVallysAspValThrLysLeu		
AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAGACGTCACATAATGGTAAGTAA	900	
GGAAATGCTTTACCGTGCTGTGTAAAAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTGAT	960	
AAAAGATTTAGATTTTCTTGCCCCCAAAGTAATGTTTTTCCTAAAGTGGGAAAGTAATCA	1020	
CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080	
TTTGTGTGTA AAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGCTCTTC	1140	
TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG	1200	
CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCCTTCA	1260	
CATGTCTTCCCTACTCTCTTTAAAAAGCCCTAACGAAAGGAAATCTGAAATGGCTATTCTC	1320	
CCAATTCAATTAGCAGGAAGACCCCTGTGCACATGTCAGTGGGTGTTGCTCCTTCAGGGAA	1380	
CATAGAGAGGCTTATTCATTGCCCCACATGTTGAAGGGACTCATCTCCCTGGTTGTGCACAT	1440	
TGAACCTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCCC	1479	
Intervening sequence of unknown length		
GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACTCAGTAGGT	60	
TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTAA	120	
TTTTGAAGGATGCCTTTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT	180	

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACACAGTTTGTGTGCTTTCTCCAA 240
 AGCACTACAAATATGATTAAATTGATGTATAAGAAATTTCTTATGGAATTTTTTTTTTGT 300
 19
 ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
 CTCTGTAGGTGGCAAAATCTTCCAAAAGACTACATGATAACCCCTCAAATATGTCCCCGGGA 360
 39
 etAspValLeu
 TGGATGTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA 420
 TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTGAG 480
 GATTGGAAGAATTTATCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT 535

FIG. 15D CONT.

Intervening sequence of unknown length

CCTGTTACAAATTCCTCCTCCTATTACAATAGTCCCTCCTCCTCCTGTGCACACTAGTC 60
 CCTTCCTCTTCTGTTACAATAACCCCTGTCCCTCCTATTACAACATTTTAAAGTAATGTAAT 120
 ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTTCATGCTTGTAAATCCCAGCACATTTGGG 180
 AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCCTGGCCCAACATGGT 240
 GAAACTTCCTCTCTACTAAAAATAAAAAGTAGCCAGGCATGGTGGCAGGCACCTTGTAAT 300
 CTGAGCTACTCGAGAGGCTGAGGCAGGAGAATCAGTTGAGTAACATAAACGATAGCTTTG 360
 AAGAGTACTCCGAGTTTATGGCACTTACTTATTAAATAGCTGTTTGTCTCTTTTTC 420

FIG. 15D CONT.

```

40                               50
ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL
ATATCTTGACGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCT 480

60                               70
euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATATTATCCATCA 540

80                               90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGGGTGAAAGAAACTCATCTA 600
96
ys
AGGTAACCTTGTGTTTCATTGGGATTATTTTTTCATTACGCTTCTCTAAAAACCCATGCTTC 660
TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTATGATATTTTGATTGTATAAACTTC 720
AAATTTAAAAATCTTGTTCAGATGAGCAAGAAACAAAGTATTTGCAGTTATATACTGCAAT 780
ACTGAAGTGCACATTC 796

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAAACCTTGTGATCCCACTGGGATCACTACCCCTGCATTACC 60
AATCTGAATTACATAACGTTAAAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA 120
CTTGAATCTTTGAGAGACATATTATATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA 180

97
AspLeuLysLysSerPheLysSerP
CTATTTGAAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAAAATCATTCAGAGCC 240

```

110 120
roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA 300
CAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAAATTTTAAATAGATCCATTGATG
130 140
laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS 360
CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGAATGTGTGGTTCTTCAACACATTAA
148
erProGluLysA 420
GTCCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAACAACAACCTTAAA
480
TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTGTTAAGCTGTAGCAAGATACATGCATGTA
541
CGTCTAATAAAAAAGCAGATATCAATAGCACAGAGAAGAACTAATGATTGTAGATTTGTGGG

Intervening sequence of unknown length

sps 60
CTCTATAACTCAATACAAATCACCATATAACACTGACACATTTATTGCTTCTTATTAGATT
150 160
erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA 120
CCAGAGTCAGTGTCAACAAAACCATTTATGTTACCCCTGTGTGCAGCCAGCTCCCTTAGGA
170 176
snAspSerSerSerSerAsnA 180
ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA
240
ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT
300
GATACTGTTCTGTACTGTATTTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT

FIG. 15D c NT.

FIG. 15D CONT.

TAAATTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTTCTGTGA 360

GGTTATTTTAAATAAGACATAAAATAATTTTAGAAATATGATTATGCCTTTTGTGAA 420

TCATTAACATATAT 434

Intervening sequence of unknown length

ACAGAAACAGTTAAACAACCCACAGCATAAGAGNAAAACCTCTAGAATGGATATGCTGTA 60

178

rgLysAlaLysAsnProProGlyAspSerSerL
TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC 120

190

200

euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG
TACACTGGCCAGCCCATGGCATTGCCAGCATTTCTTTCTTTATAAATTGGCTTTGCTTTTG 180

213

lyAlaLeu^{yl}tyr^{yl}tpLys
GAGCCTTATAC^{yl}TGGAAGGTAAGTGGTACCATTCTTTTAAAAAATATGCTATGTTTAC 240

ATAAATTATCATCTTTTTCCTCAAGAAATGATCCTTTAAGAAAAACAGTGAATCTACCT 300

TAGCTTATACTAAACAAAAATTTAAATTTTATAAAGTTTTCCTGTTTCTCATTTATGCTGGA 360

GACAAATCCCCTCTAGCTGATAATTCACGCTTAAGAAATTAGGAACT 404

Intervening sequence of unknown length

[illegible][illegible]

FIG. 15D CONT.

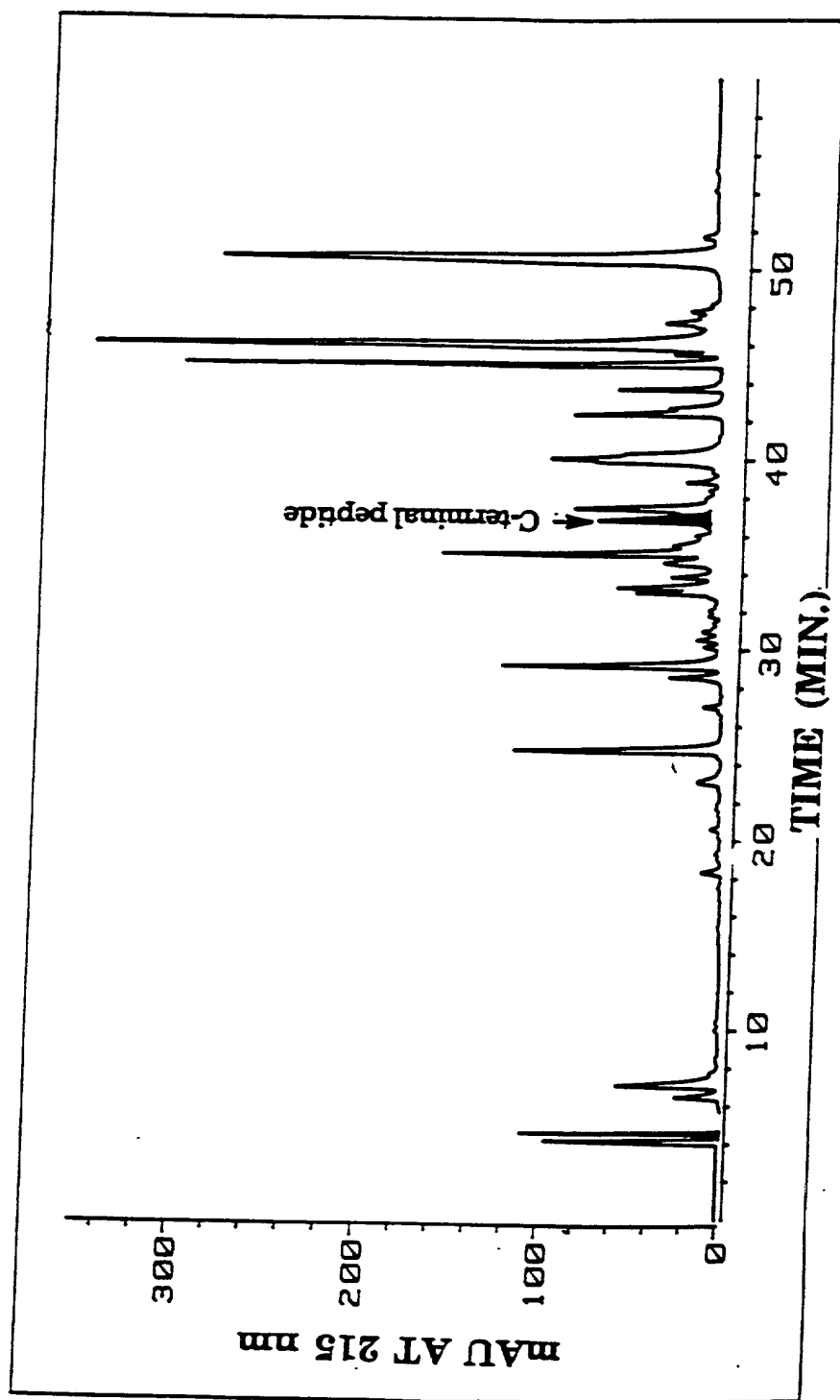
CTTTAAGTTC TAGGTTACATGTGCACAATGTGCAGGTTGTTACGTA GTTTACATGTGC 420

CATGTT 426

FIG.I6B

122	Human	SIDAFKDF.V	VASETSDCVV	SSTL.SPEKD	SRVSVTKPFM	LPPVAASSLR	169
	Monkey	SIDAFKDF.A	VASETSDCVV	SSTL.SPEKD	SRVSVTKPFM	LPPVAASSLR	
	Dog	SIDAFKDLET	VAKSSECVV	SSTL.SPDKD	SRVSVTKPFM	LPPVAASSLR	
	Cat	SIDAFKDLEM	VAKTSECVV	SSTL.SPEKD	SRVSVTKPFM	LPPVAASSLR	
	Cow	SIDAFKDLEI	VAKMSECVI	SSTS.SPEKD	SRVSVTKPFM	LPPVAASSLR	
	Rat	SIDAFKDF.M	VASDTSDCVL	SSTL.GPEKD	SRVSVTKPFM	LPPVAASSLR	
	Mouse	SIDAFKDF.M	VASDTSDCVL	SSTL.GPEKD	SRVSVTKPFM	LPPVAASSLR	
	Chicken	TIEVYKEFAD	SLDK.NDCIM	PSTVETPEND	SRVAVTKTIS	FPPVAASSLR	
	Scfpep	sIdafKdf.m	vasktSDCv	sStl.sPeKD	SRVsvTKpfm	lPPVAASSLR	
170	Human	NDSSSSNRKA	KNPPGD....	..SSLHWAAM	ALPALESLII	GFAFGALYWK	213
	Monkey	NDSSSSNRKA	KNPTGD....	..SSLHWAAM	ALPAFFSLII	GFAFGALYWK	
	Dog	NDSSSSNRKA	SNSIGD....	..SNLQWAAM	ALPAFFSLVI	GFAFGALYWK	
	Cat	NDSSSSNRKX	TNP IED....	..SSIQWAVM	ALPACFSLVI	GFAFGAFYWK	
	Cow	NDSSSSNRKA	SNSIED....	..SSLQWAAV	ALPAFFSLVI	GFAFGAFYWK	
	Rat	NDSSSSNRKA	AKSPED....	..PGLQWTAM	ALPALISLVI	GFAFGALYWK	
	Mouse	NDSSSSNRKA	AKAPED....	..SGLQWTAM	ALPALISLVI	GFAFGALYWK	
	Chicken	NDSIGSNTSS	NSNKEALGFI	SSSSLQGISI	ALTSLLSLLI	GFILGAIYWK	
	Scfpep	NDsSSsNrka	.n..ed....	..sslqwaam	AlpalfSLVI	GfAfGALYWK	
214	Human	KRQPSLTRAV	ENIQIN...E	EDNEISMLQe	KEREFQeV		248
	Monkey	KRQPSLTRAV	ENIQIN...E	DDNEISMLQe	KEREFQeV		
	Dog	KKQPNLTRTV	ENIQIN...E	EDNEISMLQe	KEREFQeV		
	Cat	KKQPNLTRTV	ENIQIN...E	EDNEISMLQe	KEREFQeV		
	Cow	KKQPNLTRTV	ENRQIN...E	EDNEISMLQe	KEREFQeV		
	Rat	KKQSSLTRAV	ENIQIN...E	EDNEISMLQe	KEREFQeV		
	Mouse	KKQSSLTRAV	ENIQIN...E	EDNEISMLQe	KEREFQeV		
	Chicken	KTHPKSPES	NETIQCHGCQ	EENEISMLQe	KEKEHLQV		
	Scfpep	Kkqpsltrav	eniqin...e	edNEISMLQe	KerEfQeV		

FIG. 16C



[illegible]

ta a t t t a a t t c g t a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
 E F F R I F N R S I D A F K D F V

BstEII
t a a c a g t c a a t t a c t . a
AAAGACTCCCGTGTTTCGGTTACCAACCGTTCATGCTGCCGCCGGTTGCT
K D S R V S V T K P F M L P P V A

BamHI

t

CTGATCTAATAGGATCC

L | * *

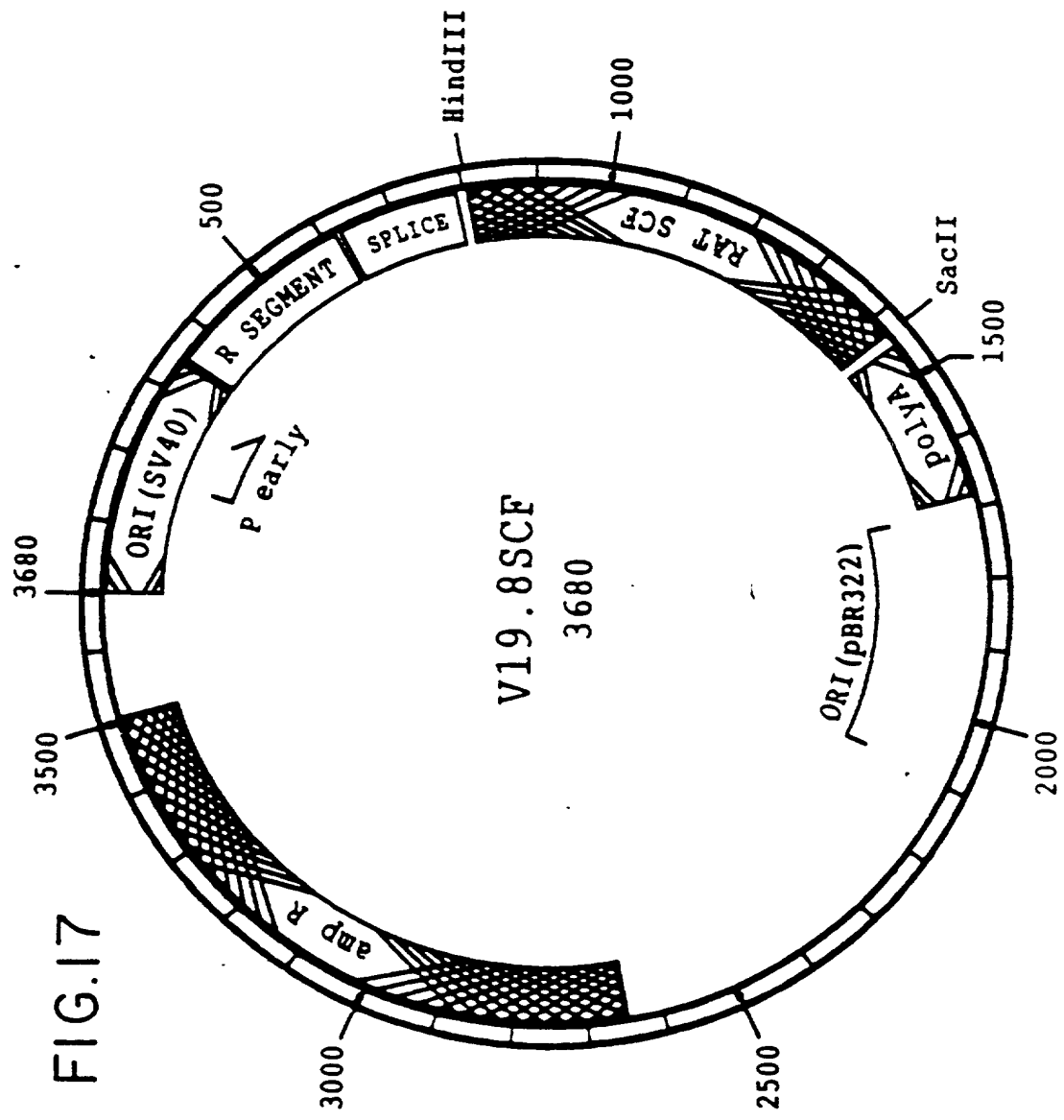
FIG 16E

BstEII
BamHI

GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC

V T K P F M L P P V A A * *

FIG.17



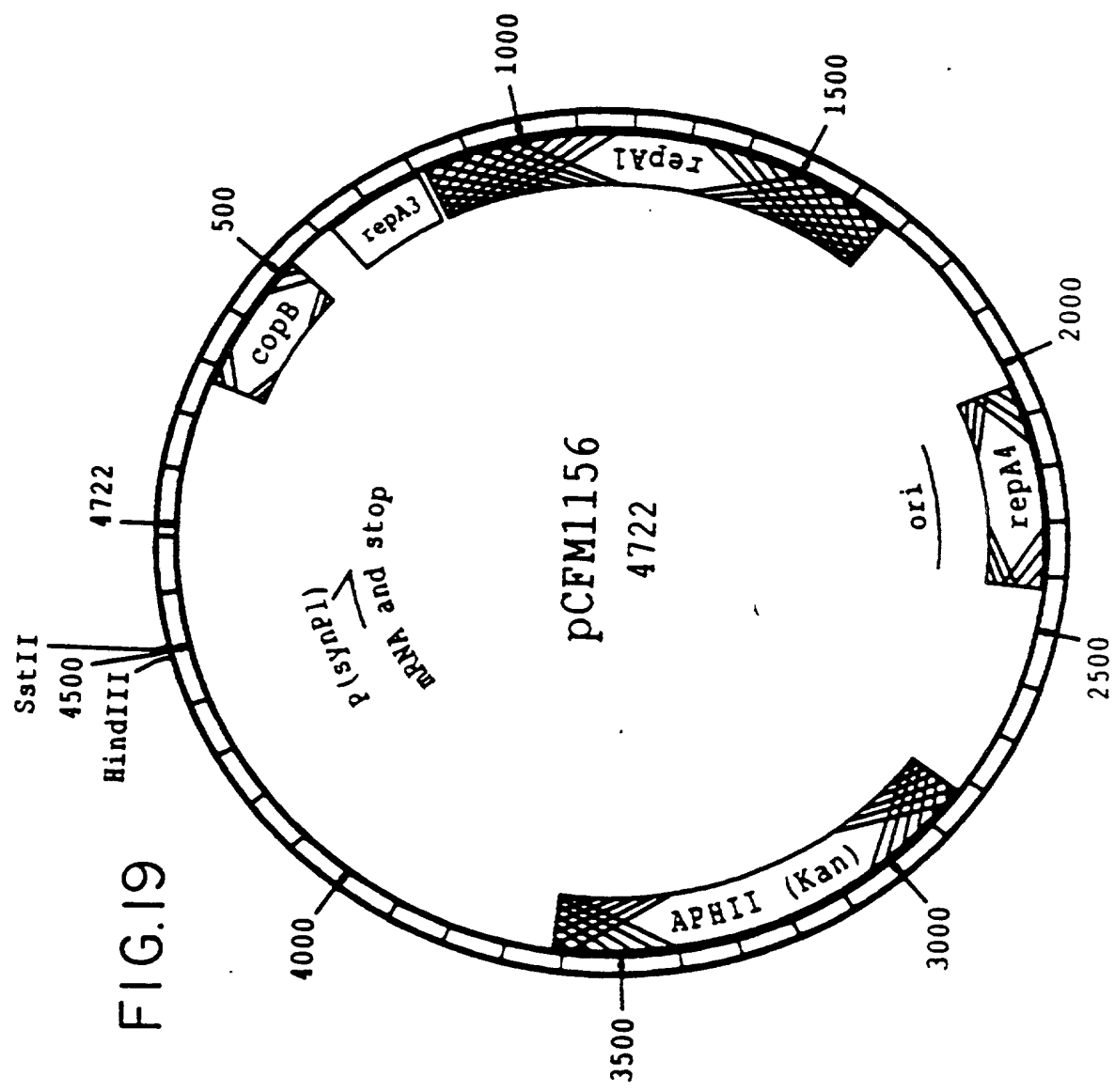


FIG.19

FIG.20A

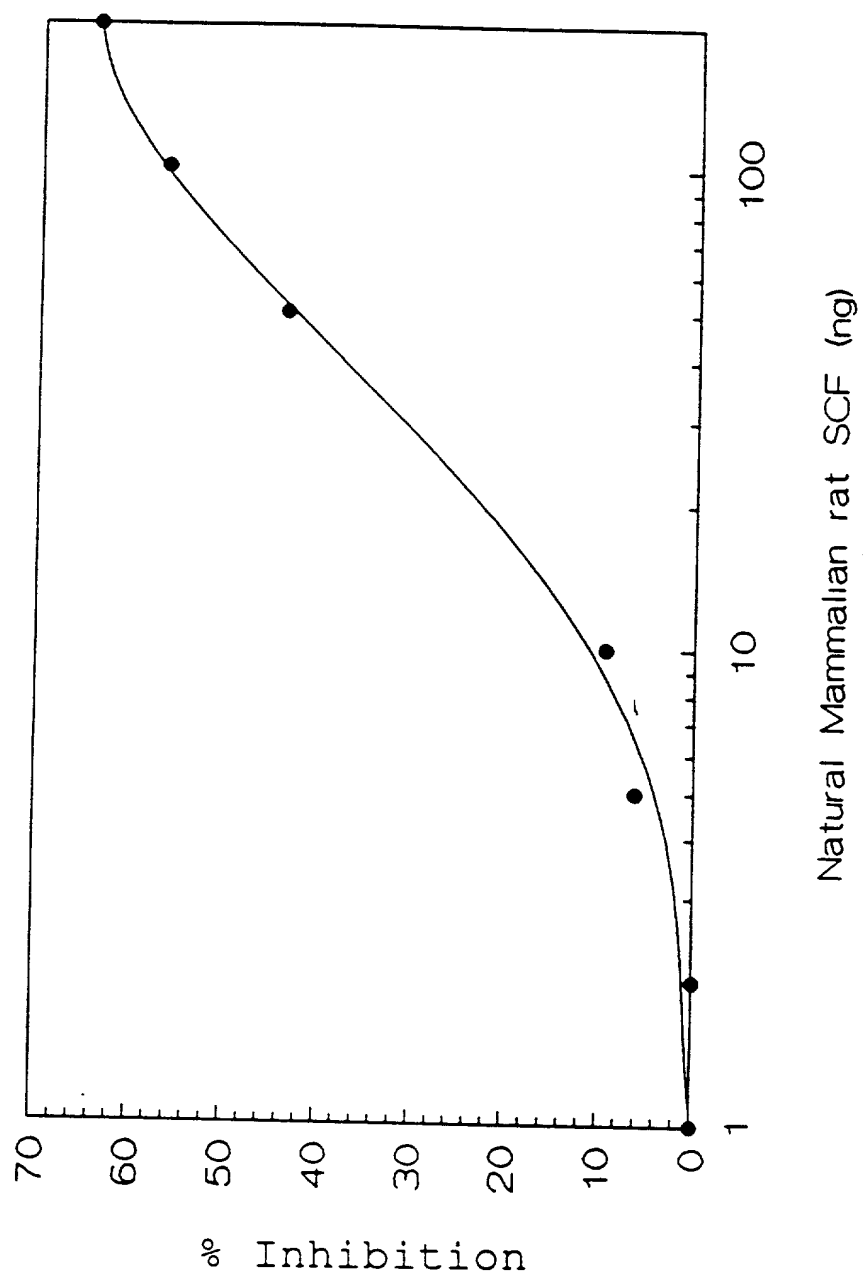


FIG.20B

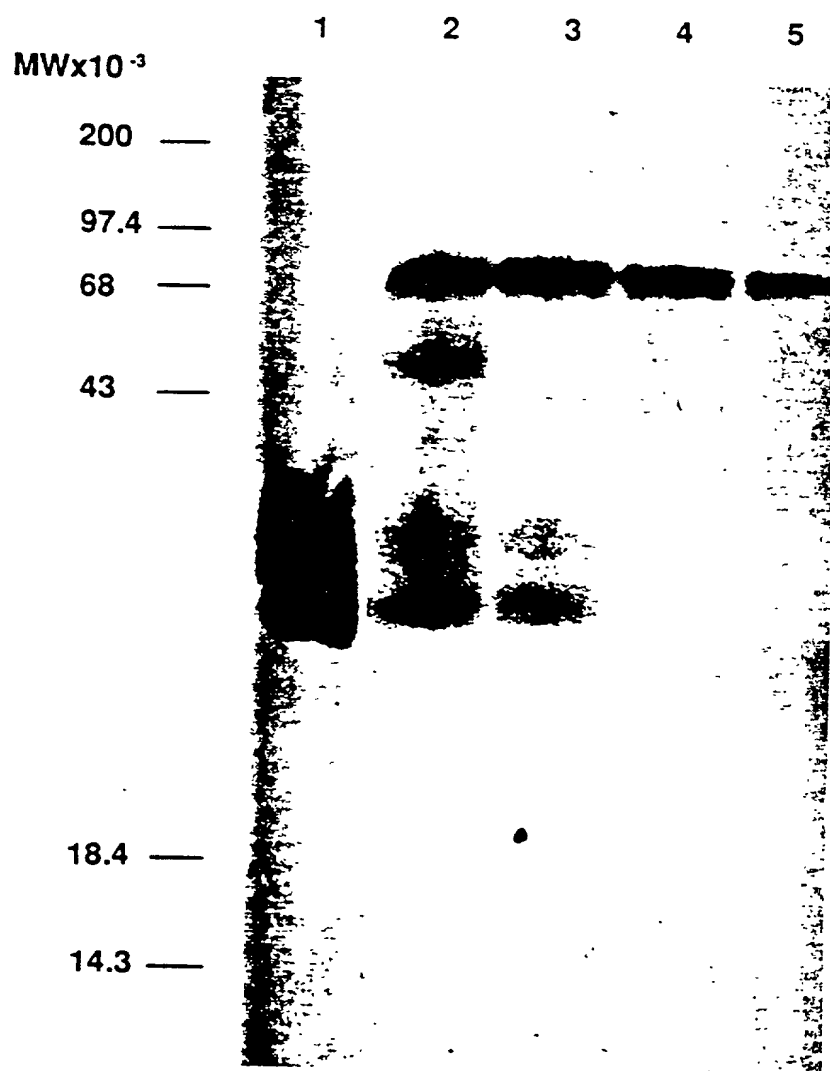


FIG. 21

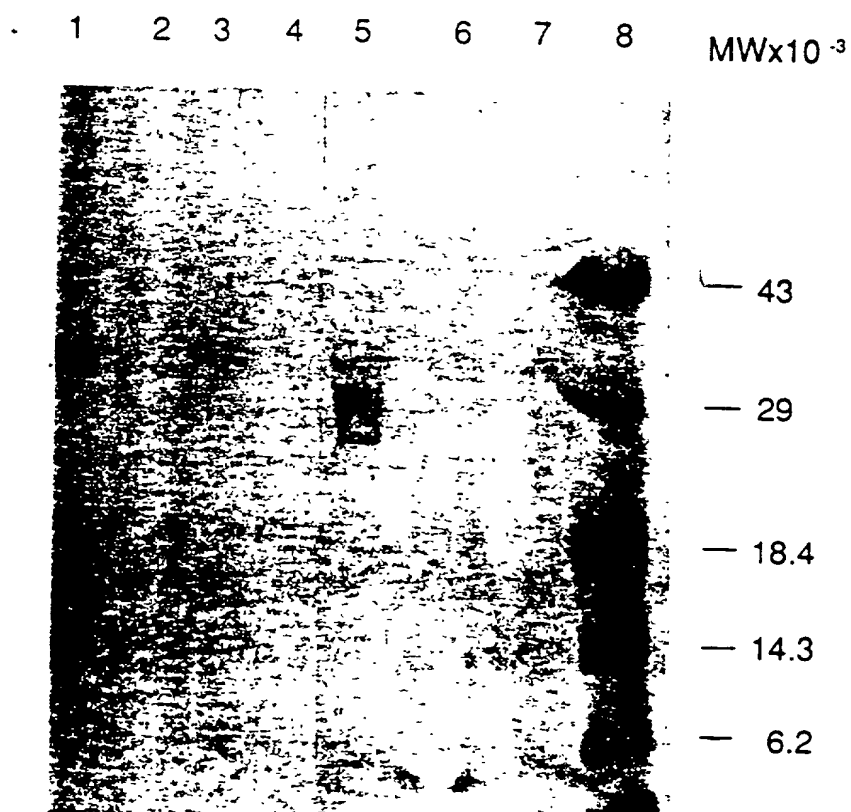


FIG.22

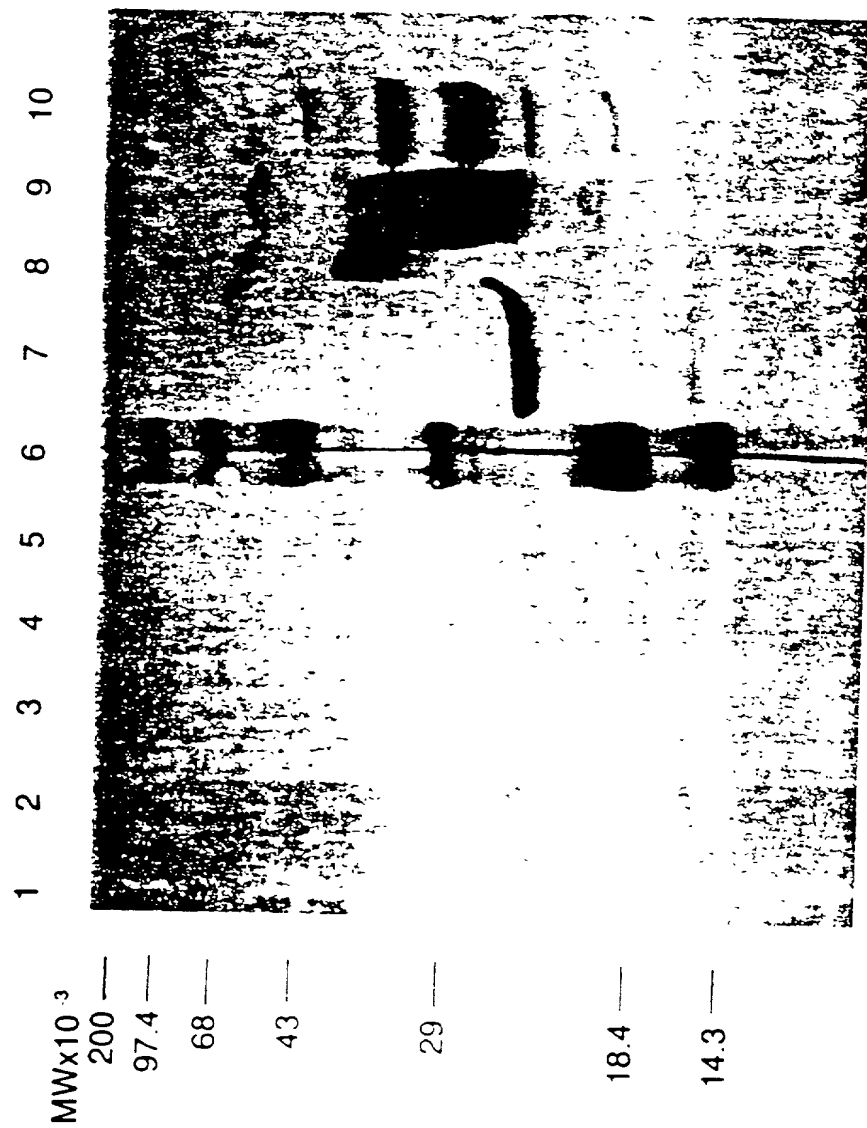


FIG. 22A

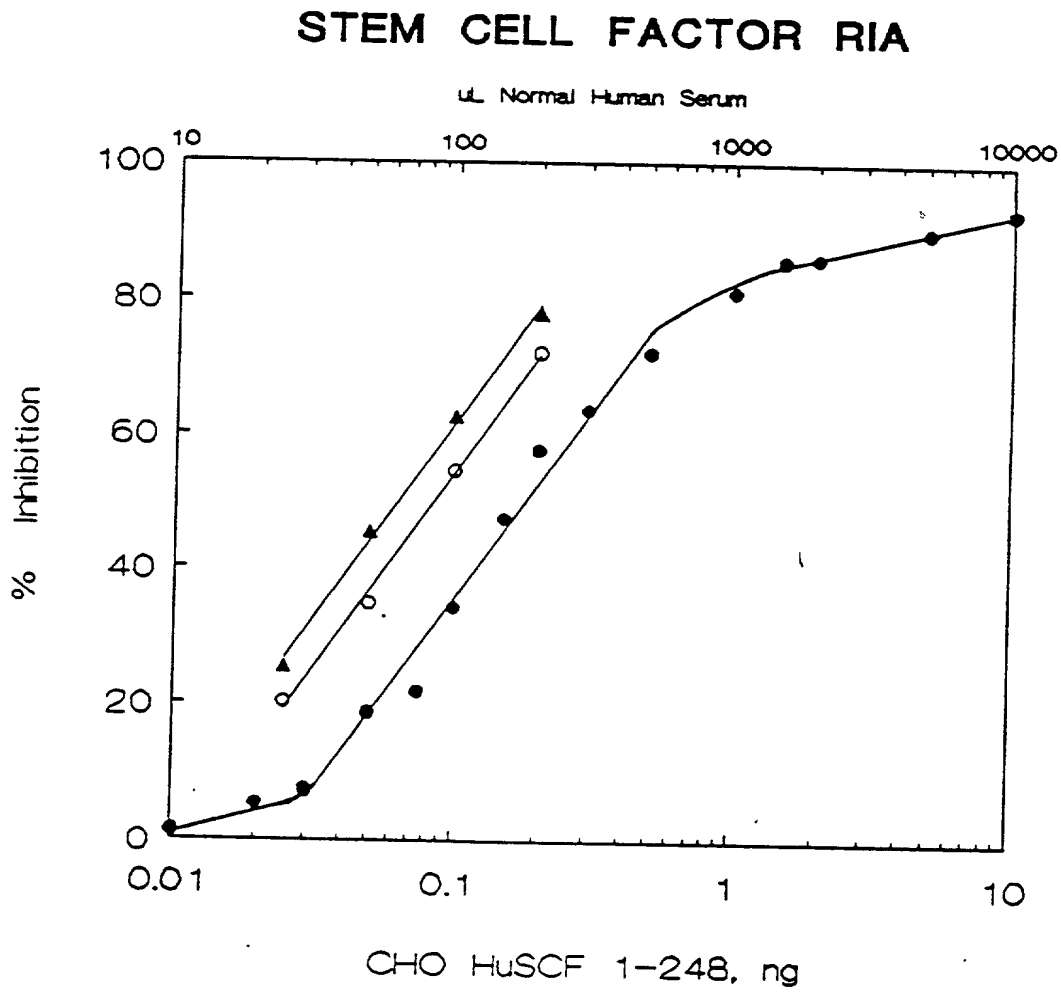


FIG. 23

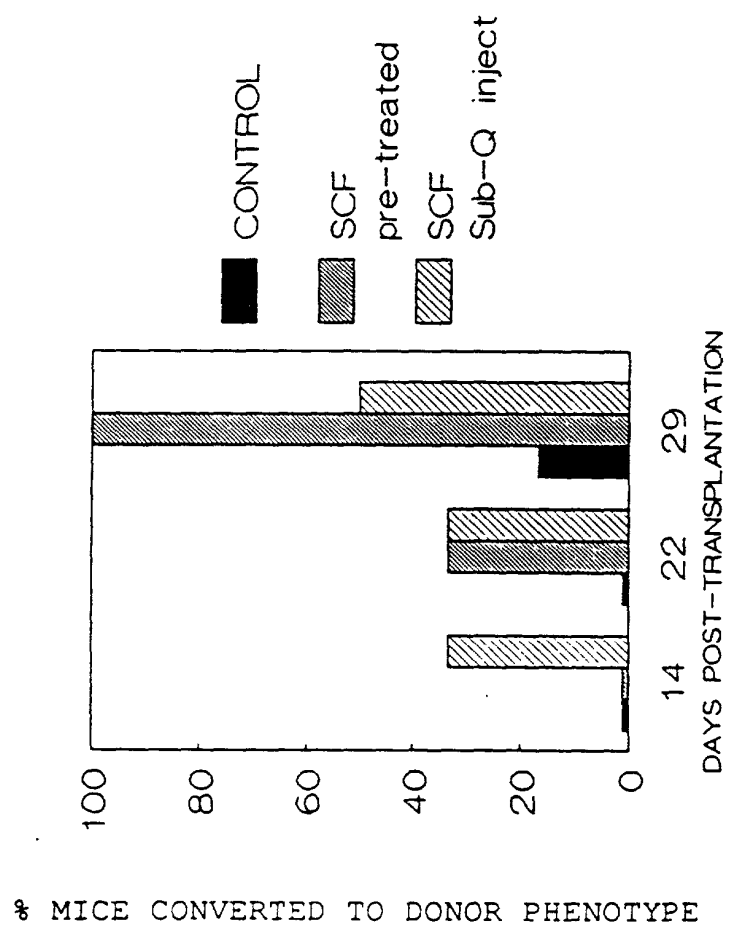


FIG. 24A

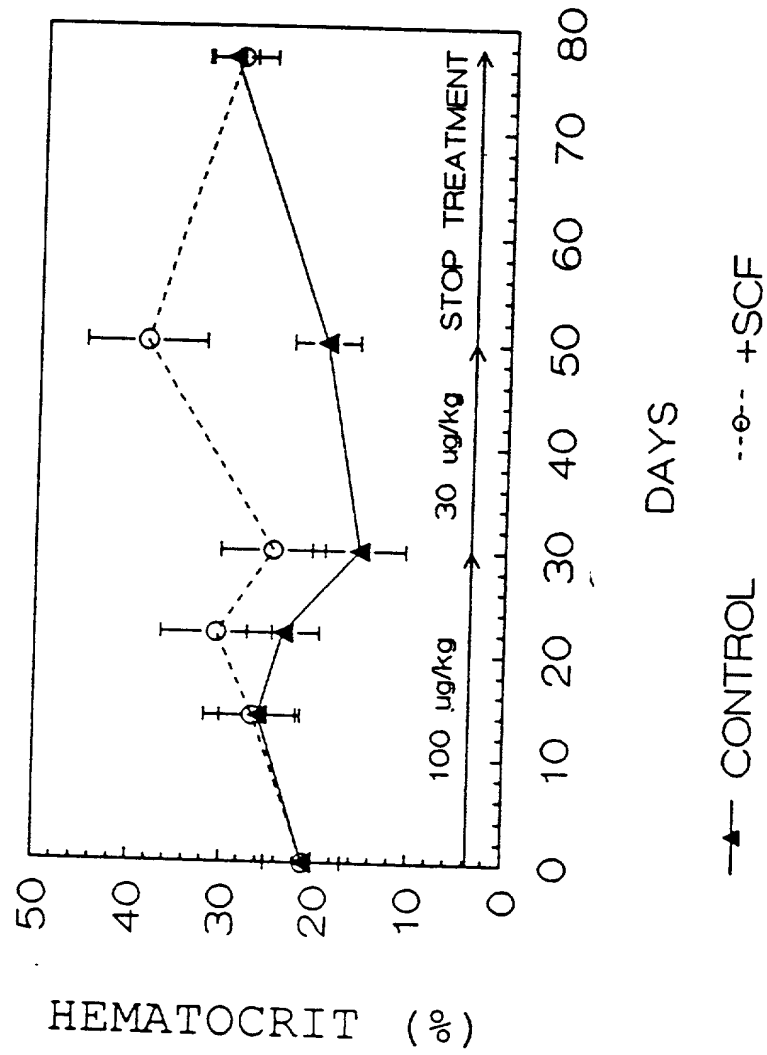


FIG. 24 B

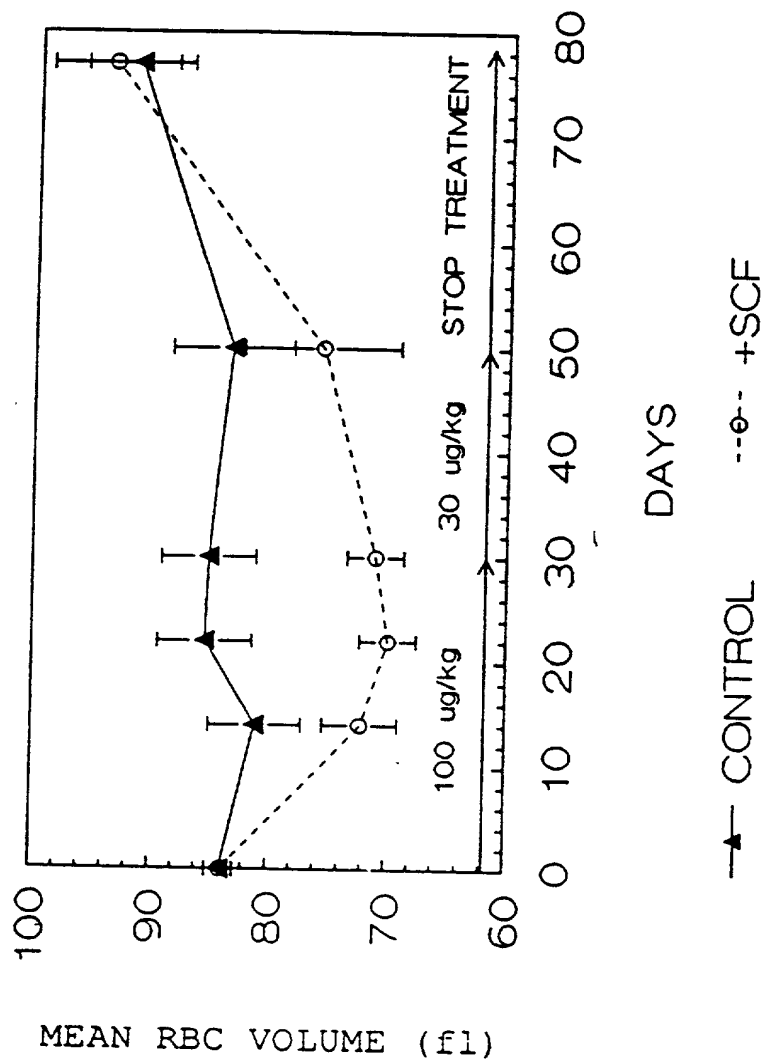


FIG. 25

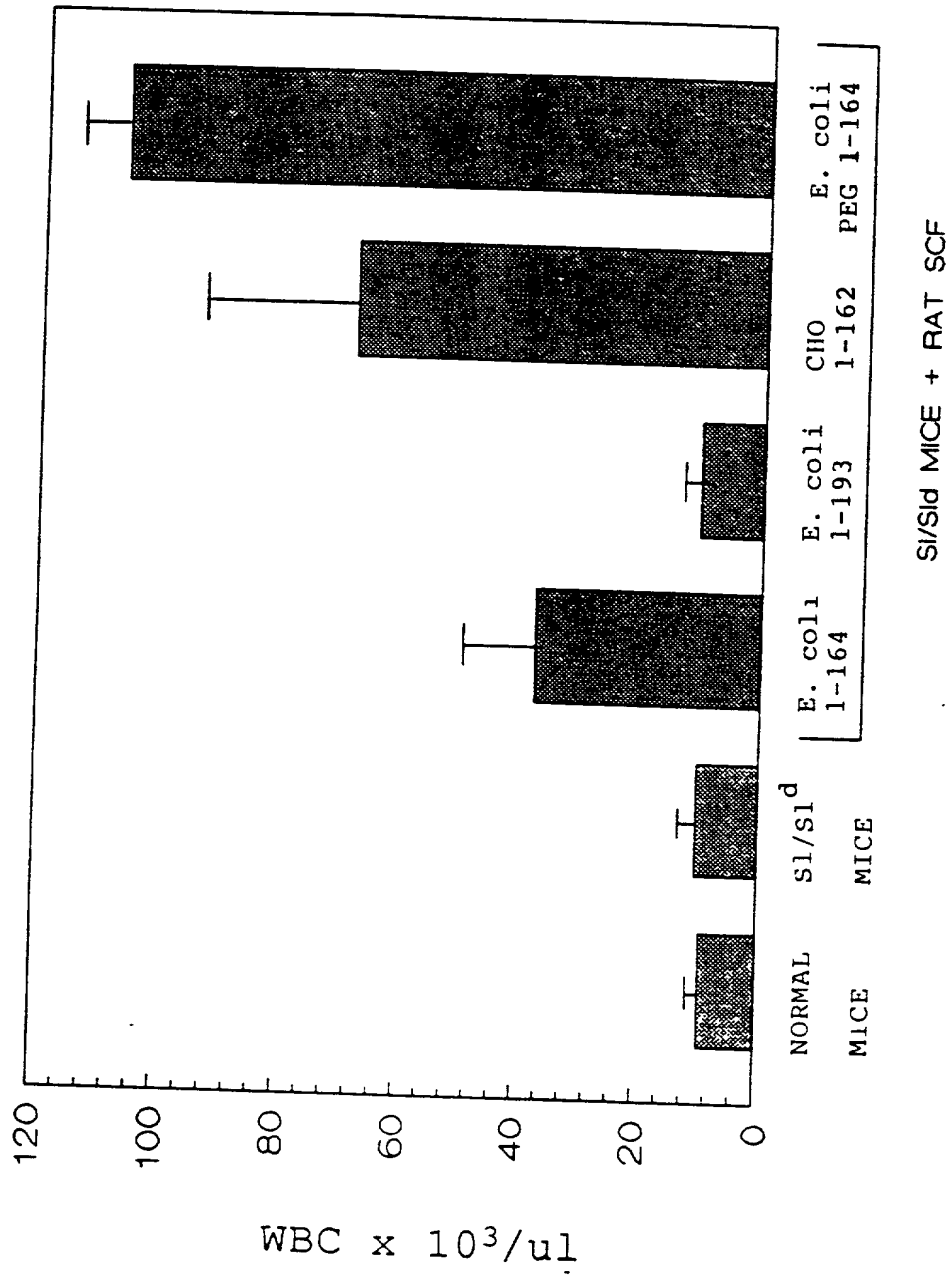
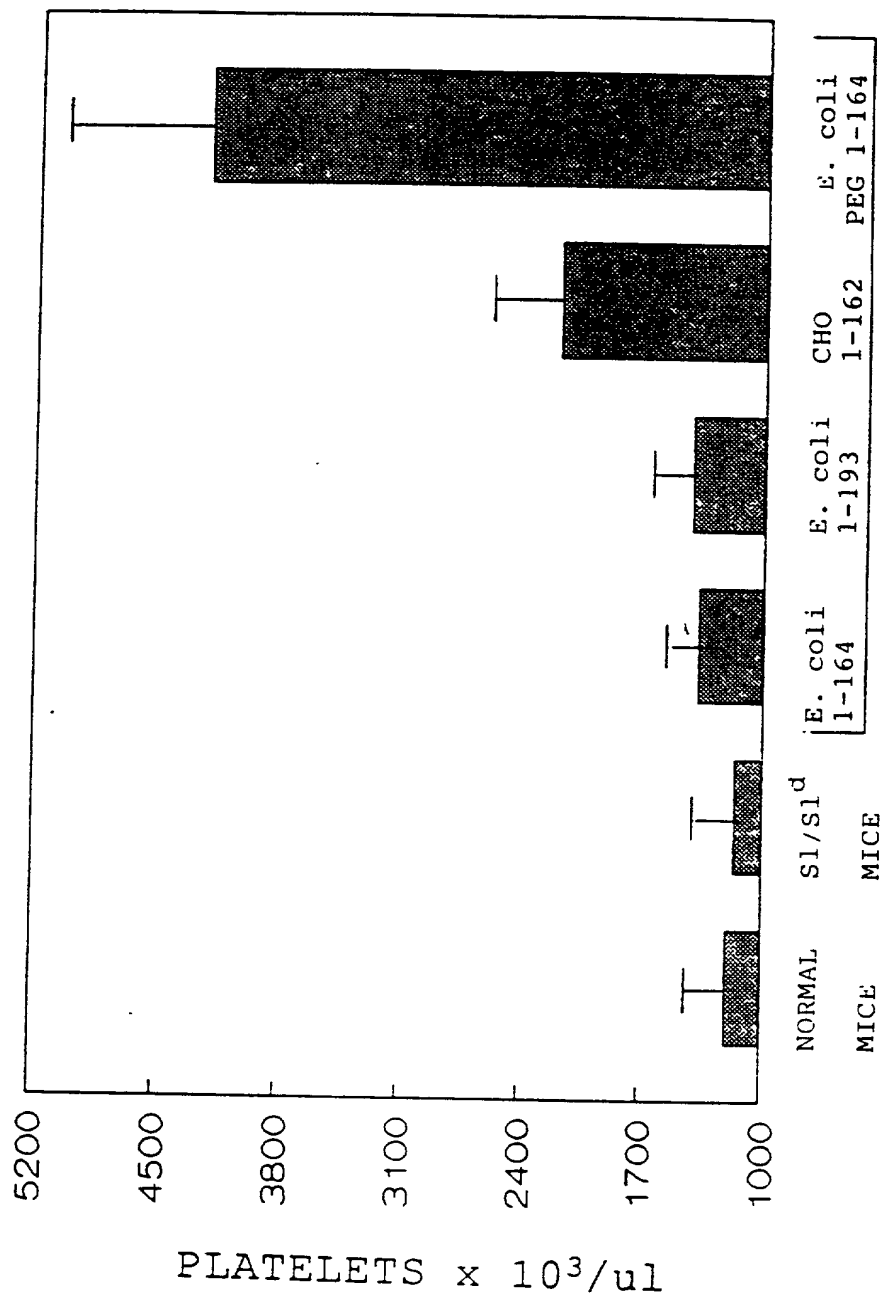


FIG.26



SI/SId MICE + RAT SCF

FIG. 27

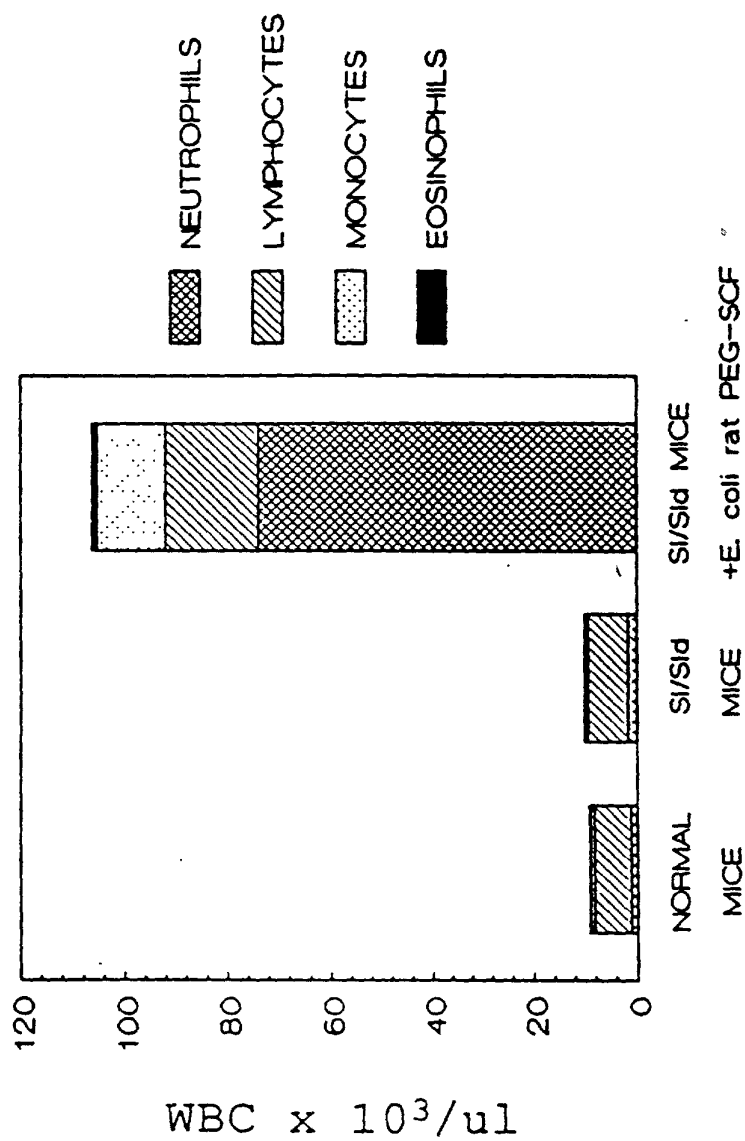


FIG. 28

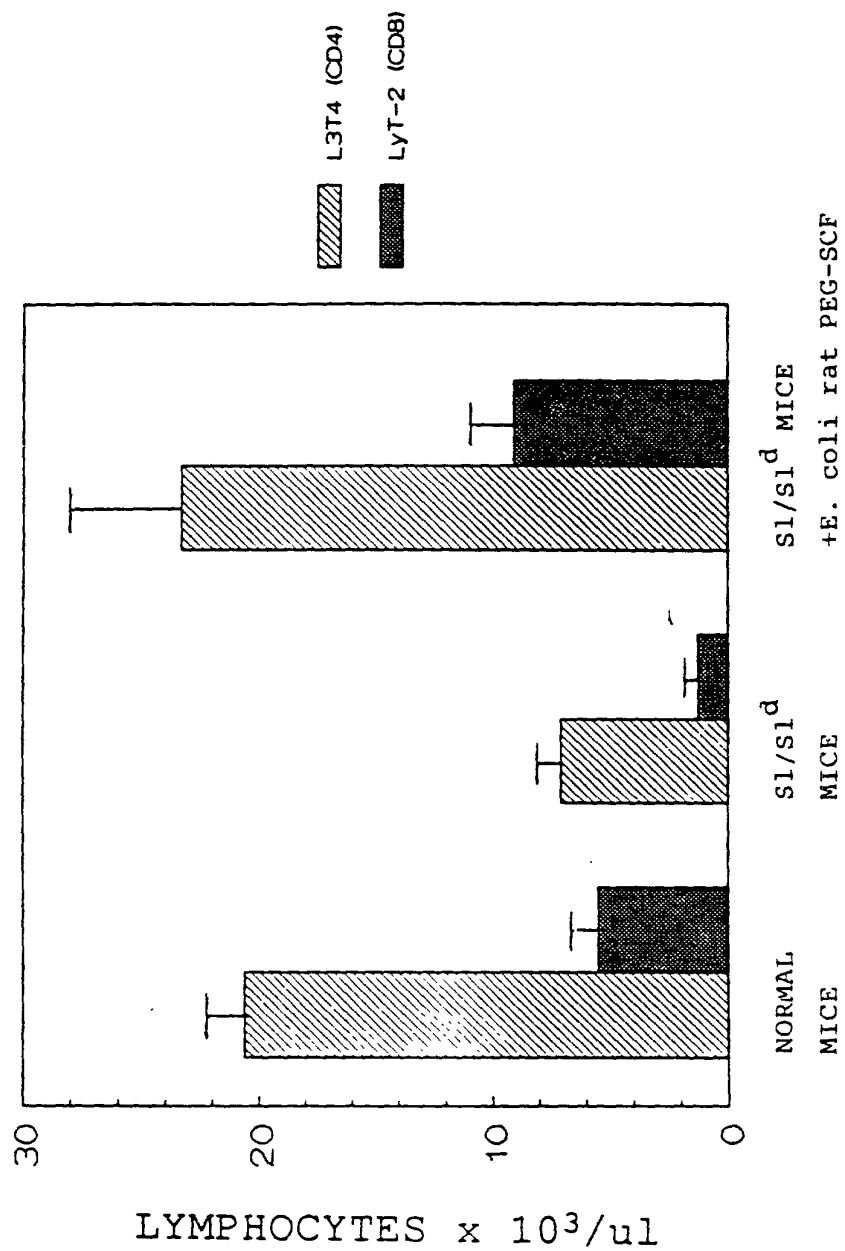


FIG.29A

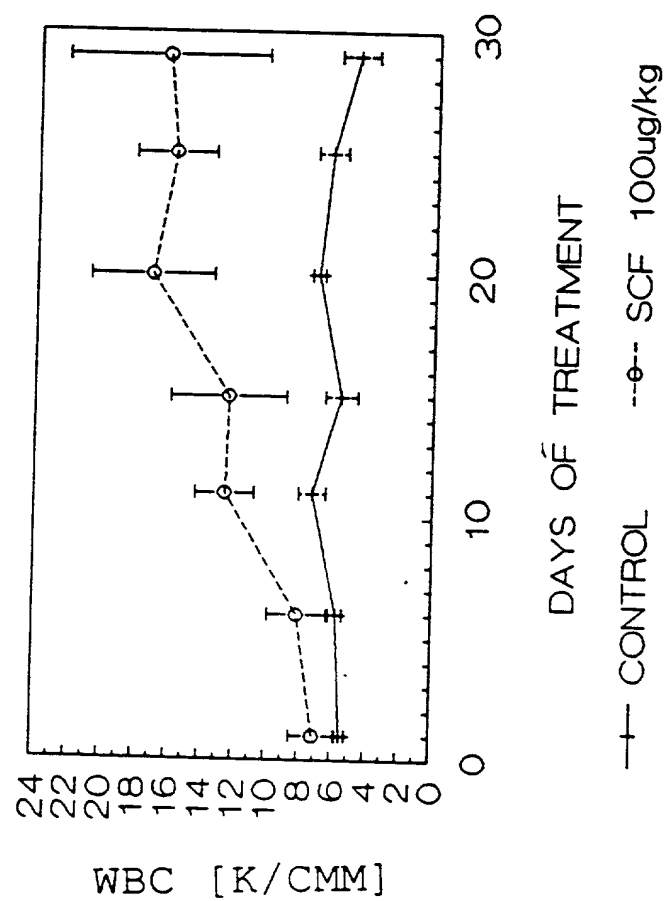


FIG. 29B

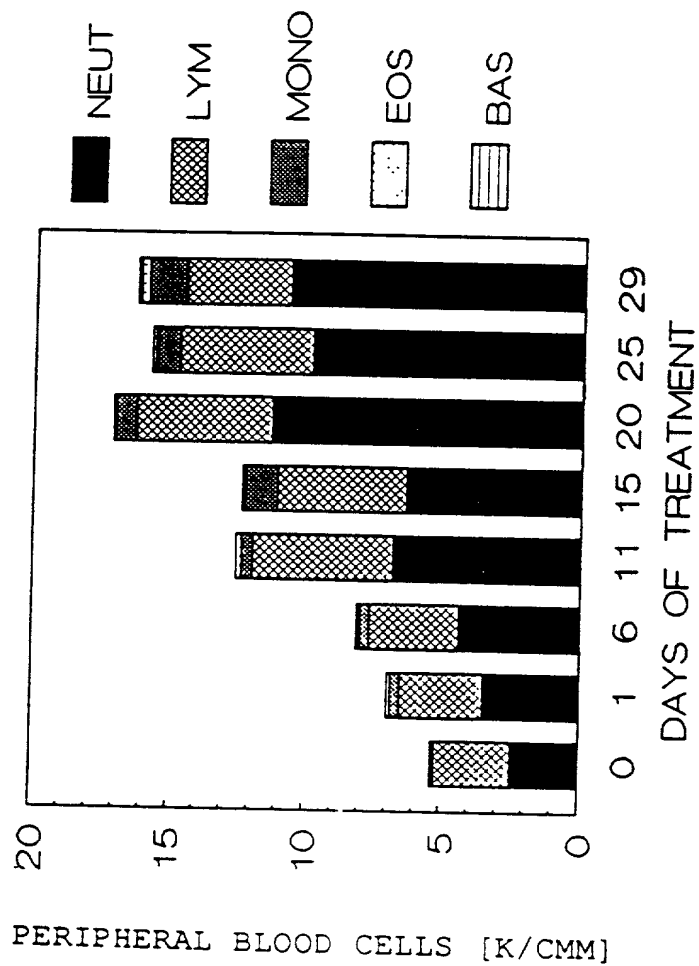


FIG.30A

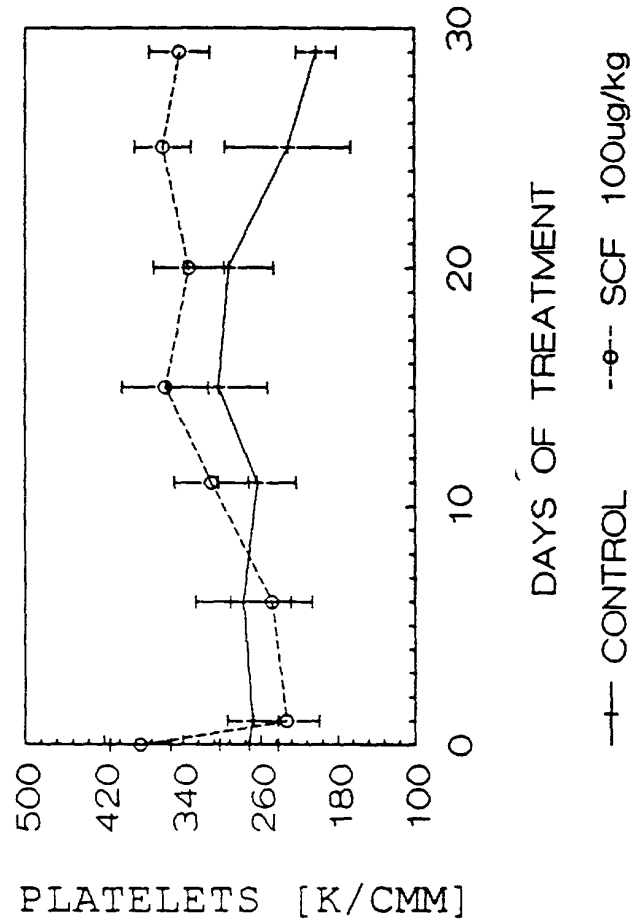


FIG.30B

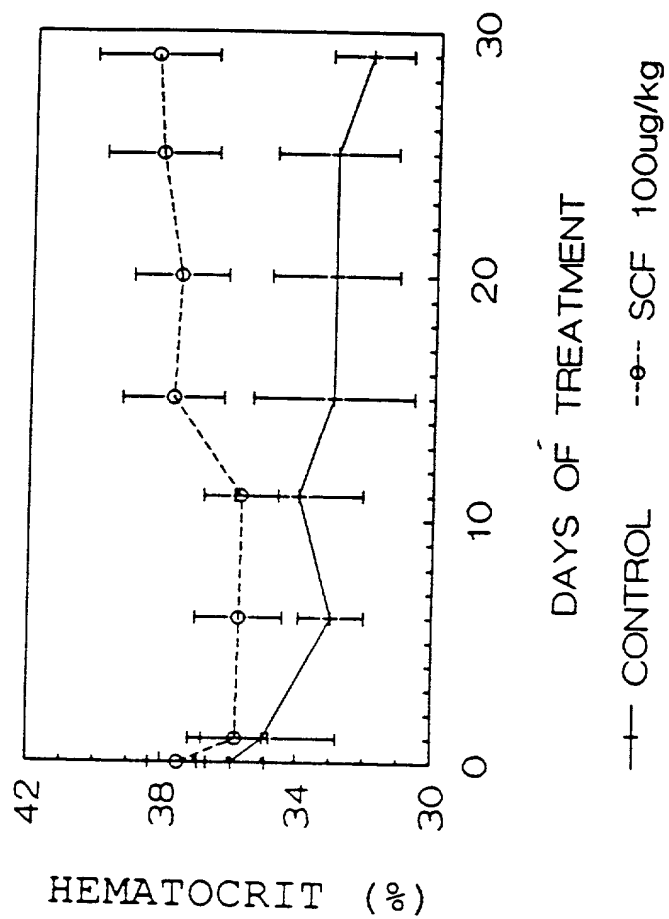


FIG. 31A

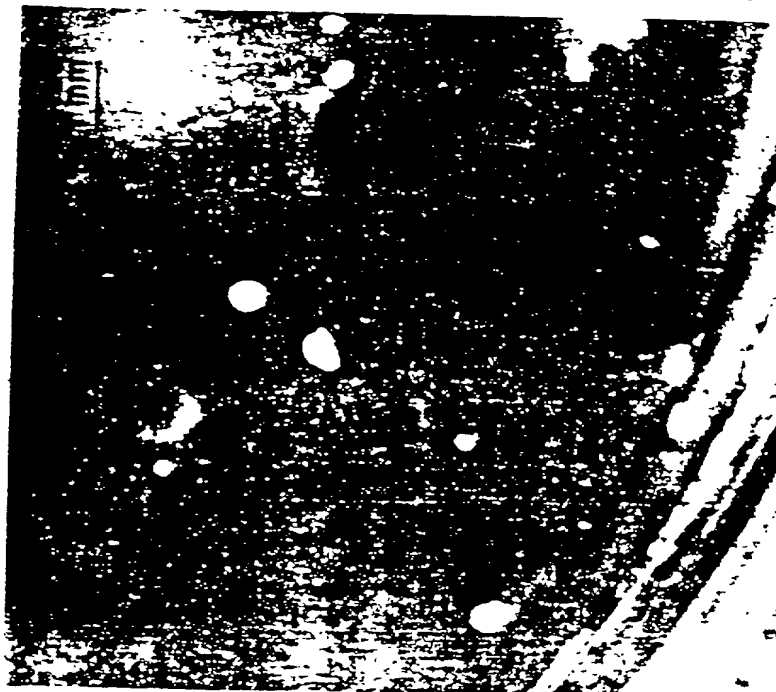
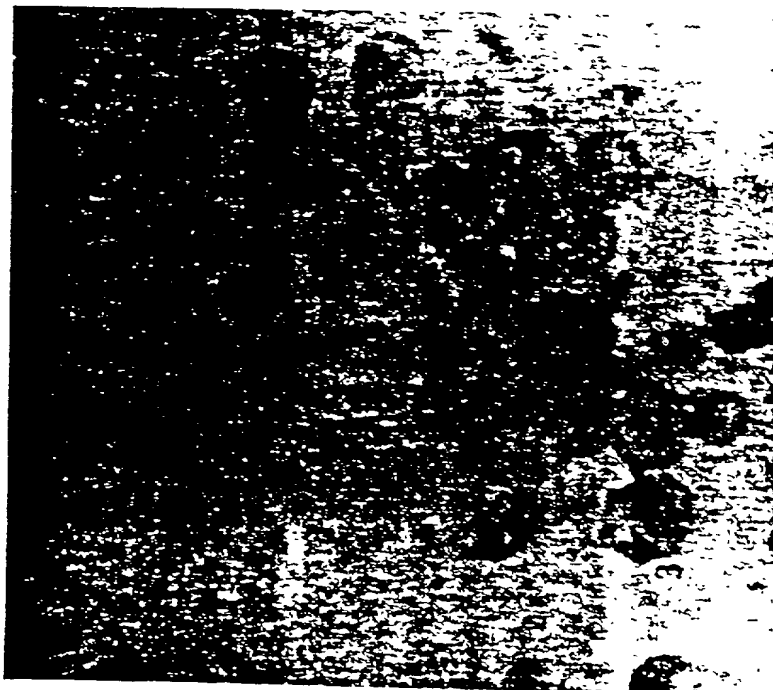
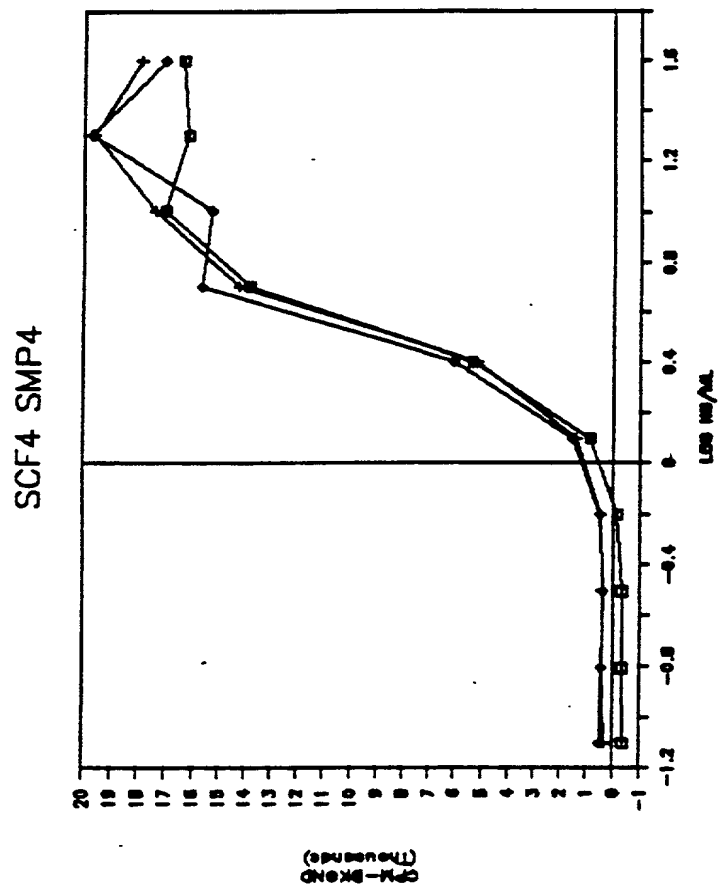


FIG. 31B



SCF4 SMP4
FIG. 31C



S Sephrose Load

FIG. 32A

11 15 19 23 27 31 35 37
13 17 21 25 29 33

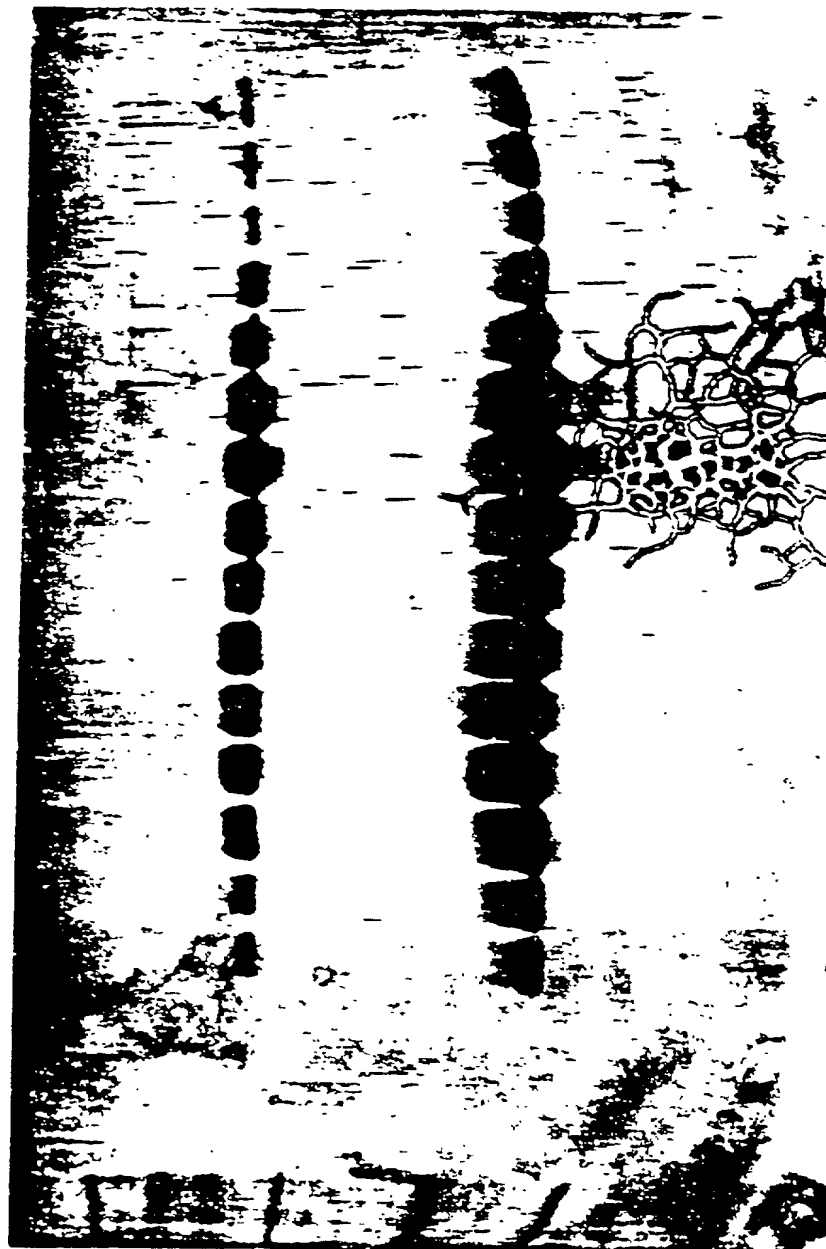


9.4 —
6.2 —
3.7 —
1.1 —
215 —
144 —

S Sephrose Load

FIG. 32 B

11 15 19 23 27 31 35
13 17 21 25 29 33 37



97 4 —
66 2 —
42 7 —
31 1 —
21 5 —
14 4 —

FIG. 33

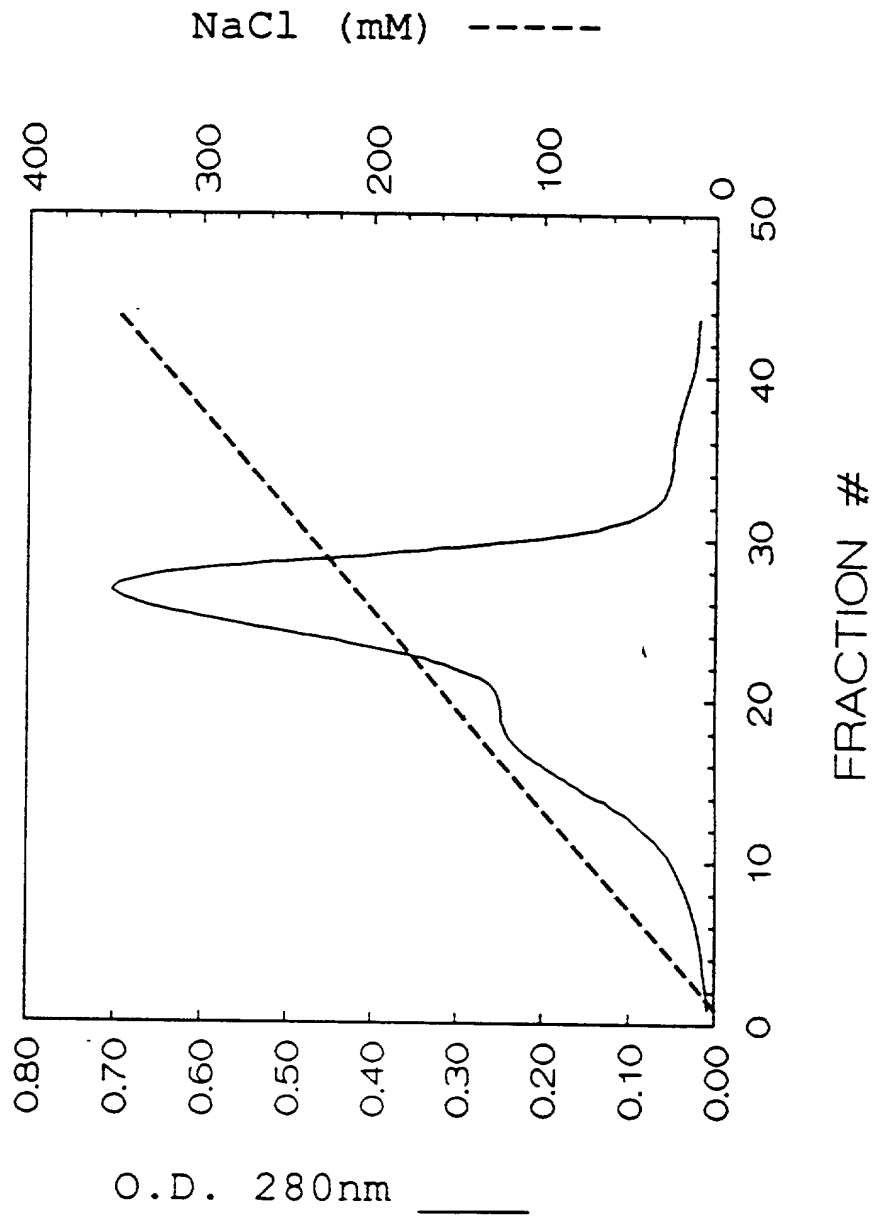


FIG.34A

S Sepharose Pool
C4 Load
C4 Flow Thru

62	76	90	104	118	132	146	160	181	201	211	221	231
69	83	97	111	125	139	153	166	181	206	216	226	



97.4
66.2
41.7
11.1
21.5
1.1

FIG. 34B

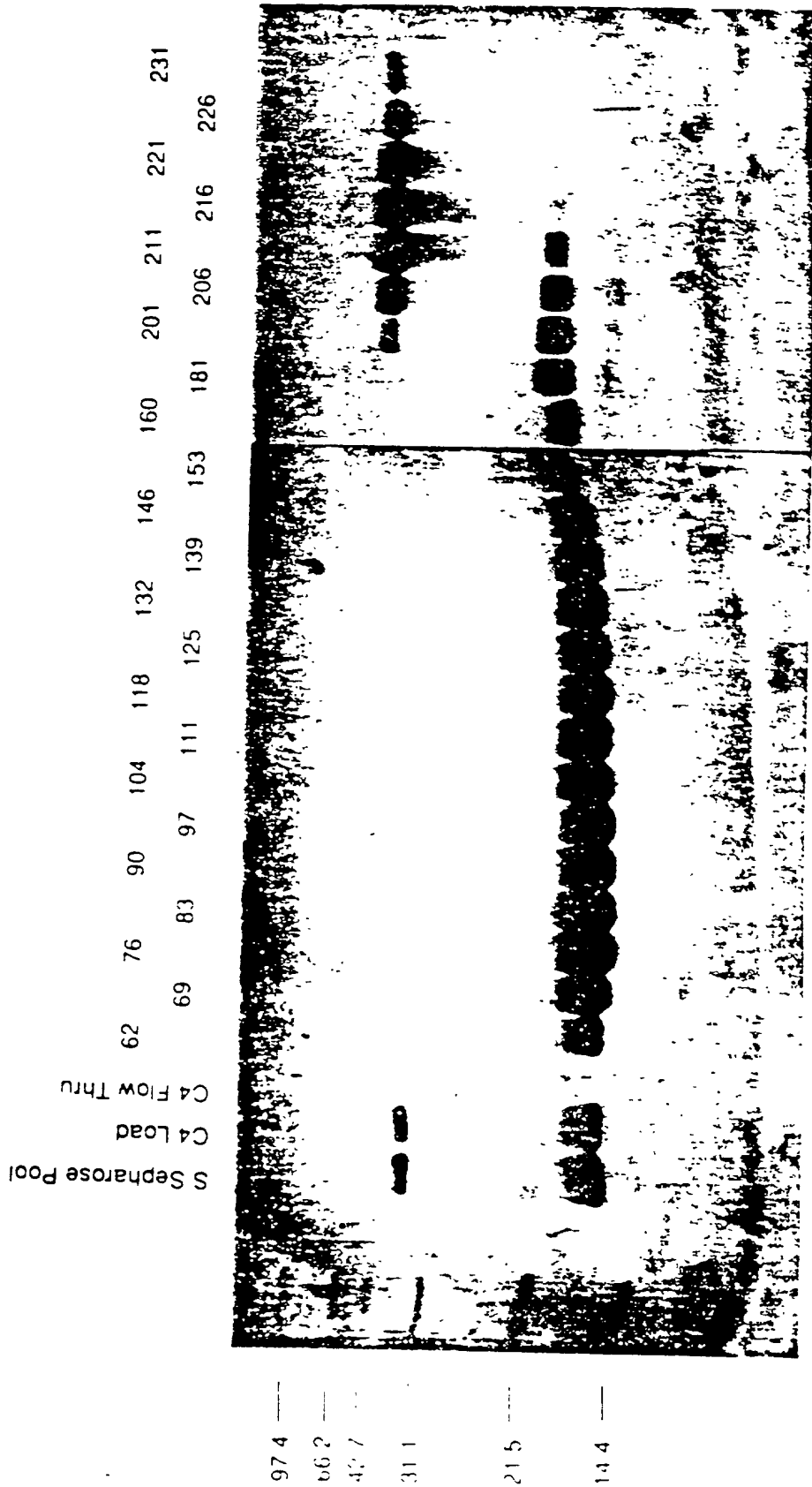
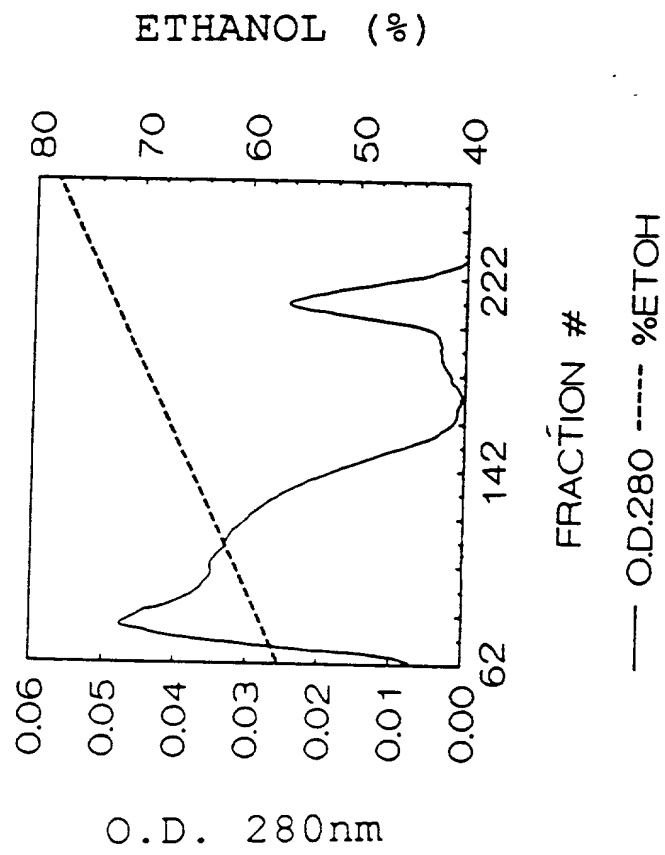


FIG. 35



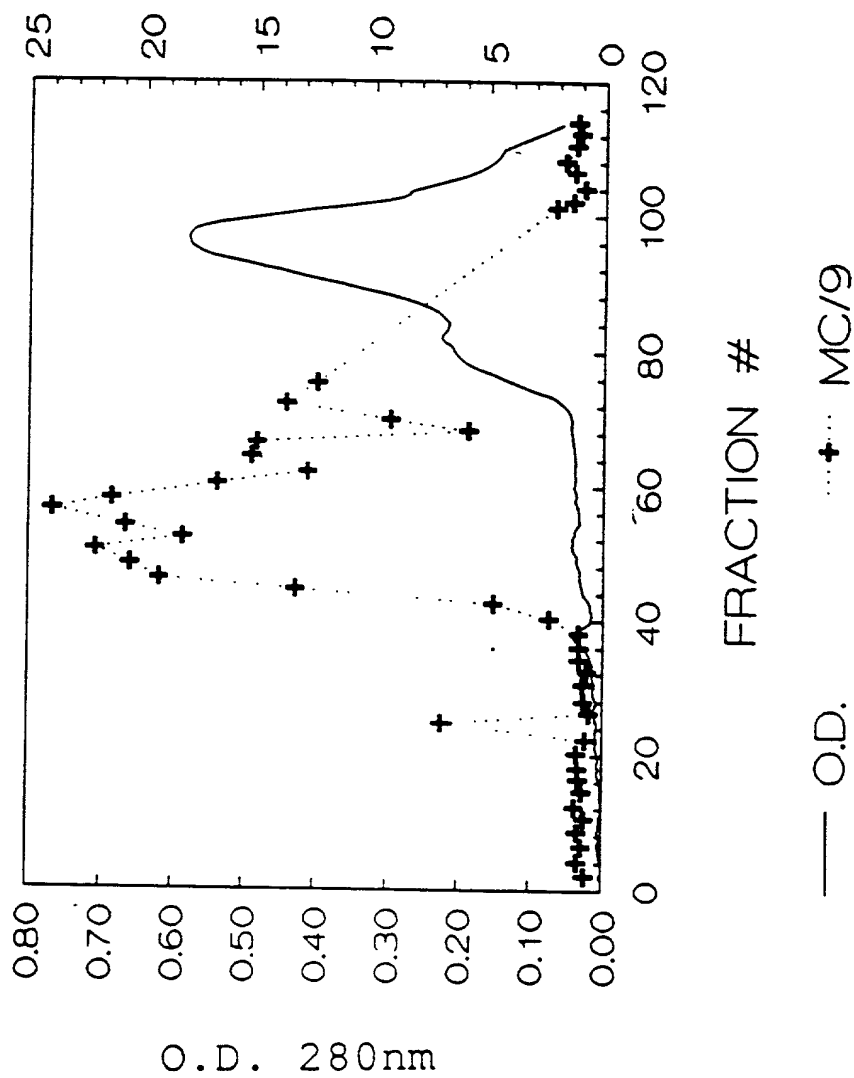


FIG. 37

MC/9 CPM ($\times 10^{-3}$)

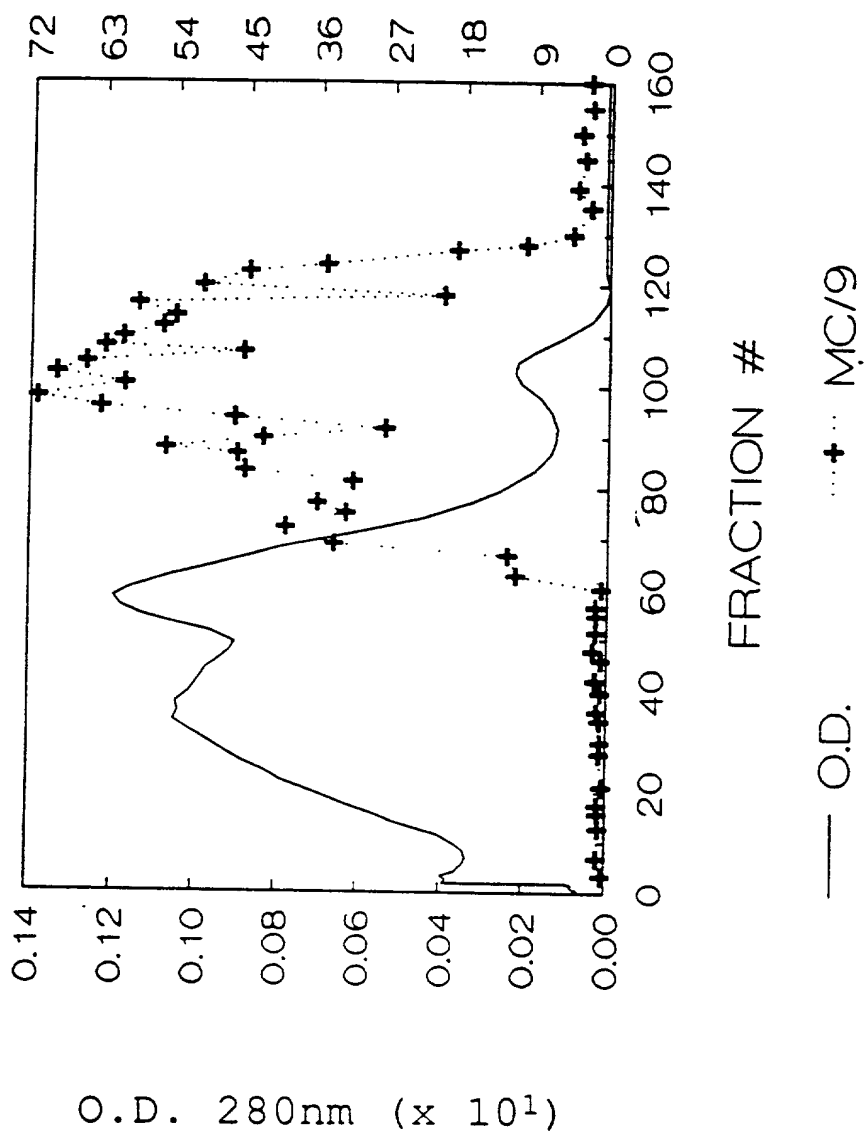


FIG.38

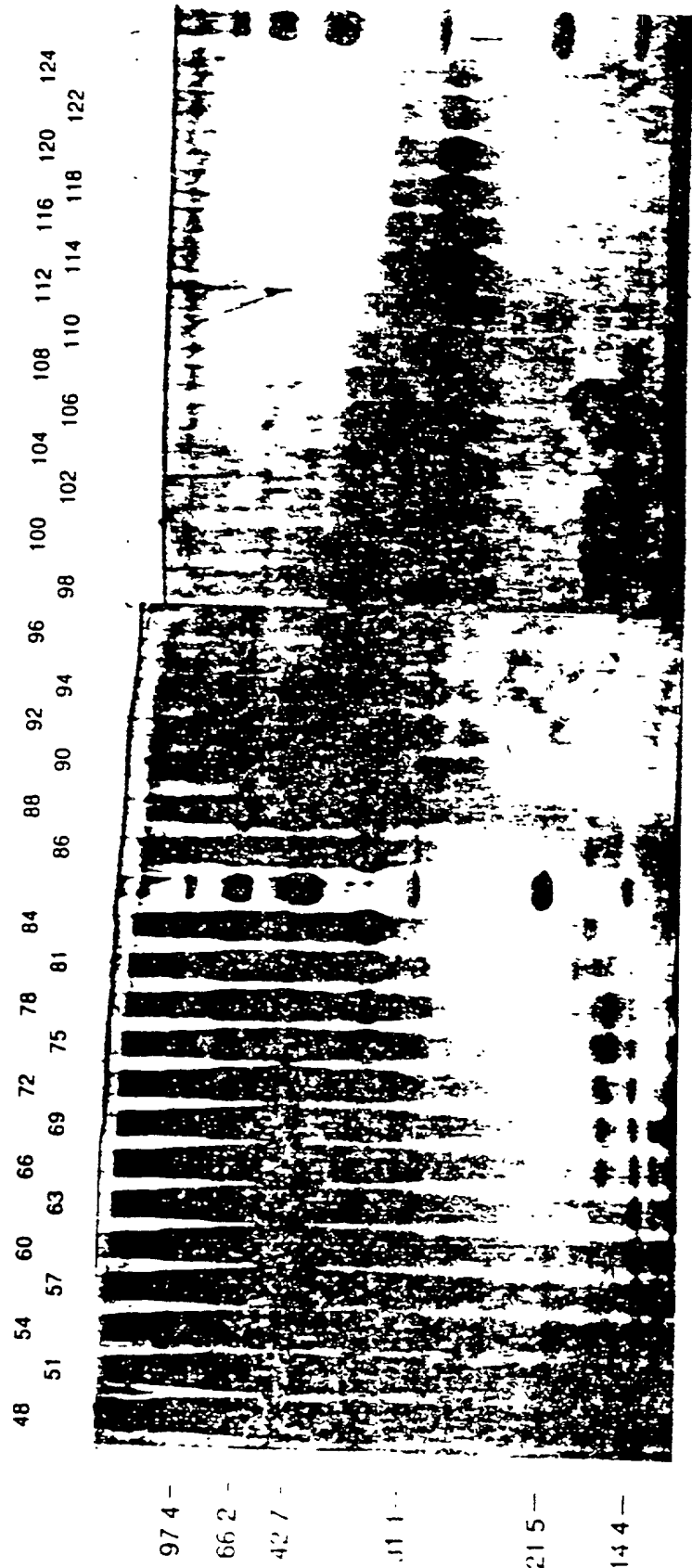


FIG. 39

1	2	3	4	5	6	7	8	9
---	---	---	---	---	---	---	---	---

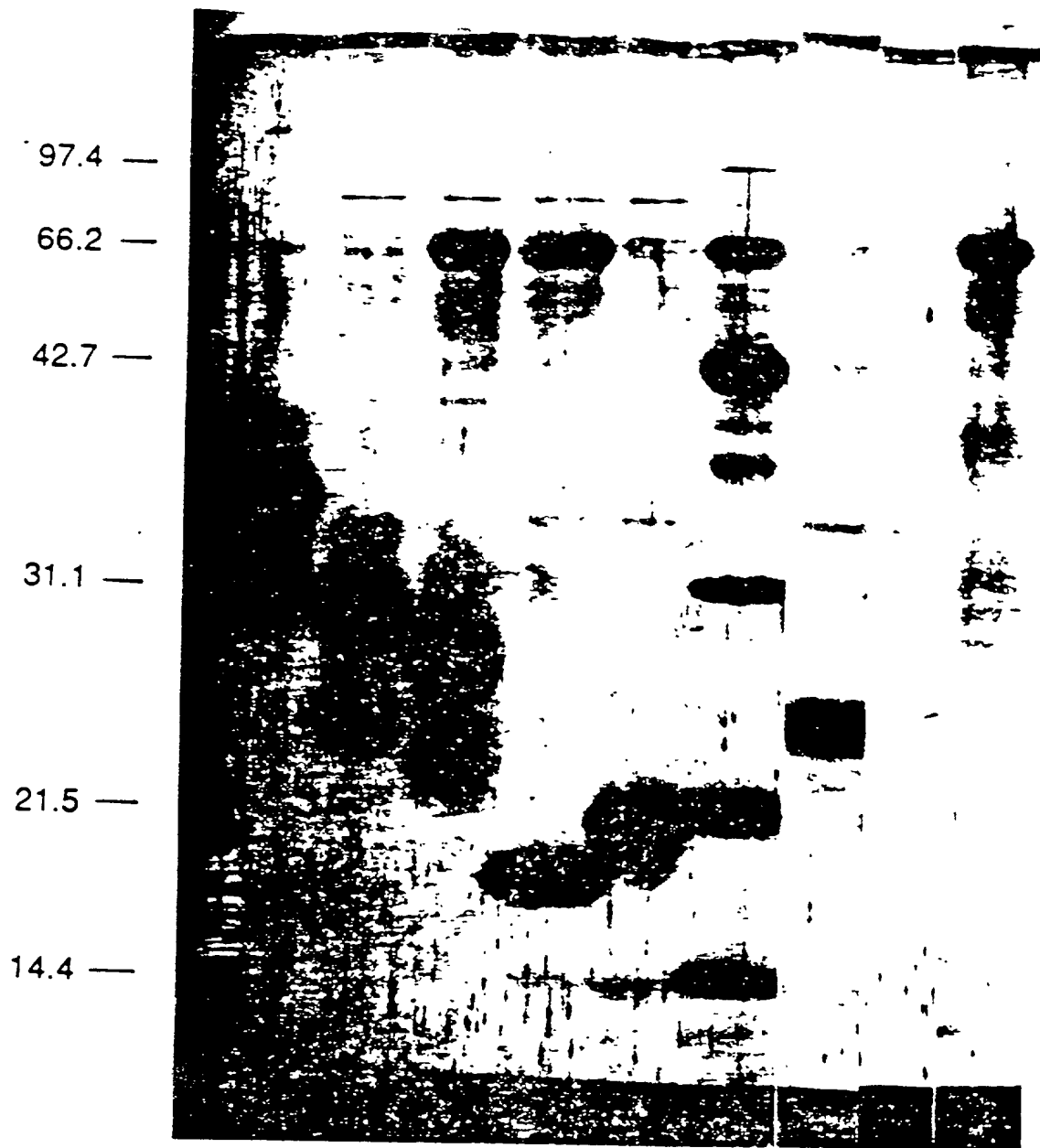
[illegible]

FIG. 40A

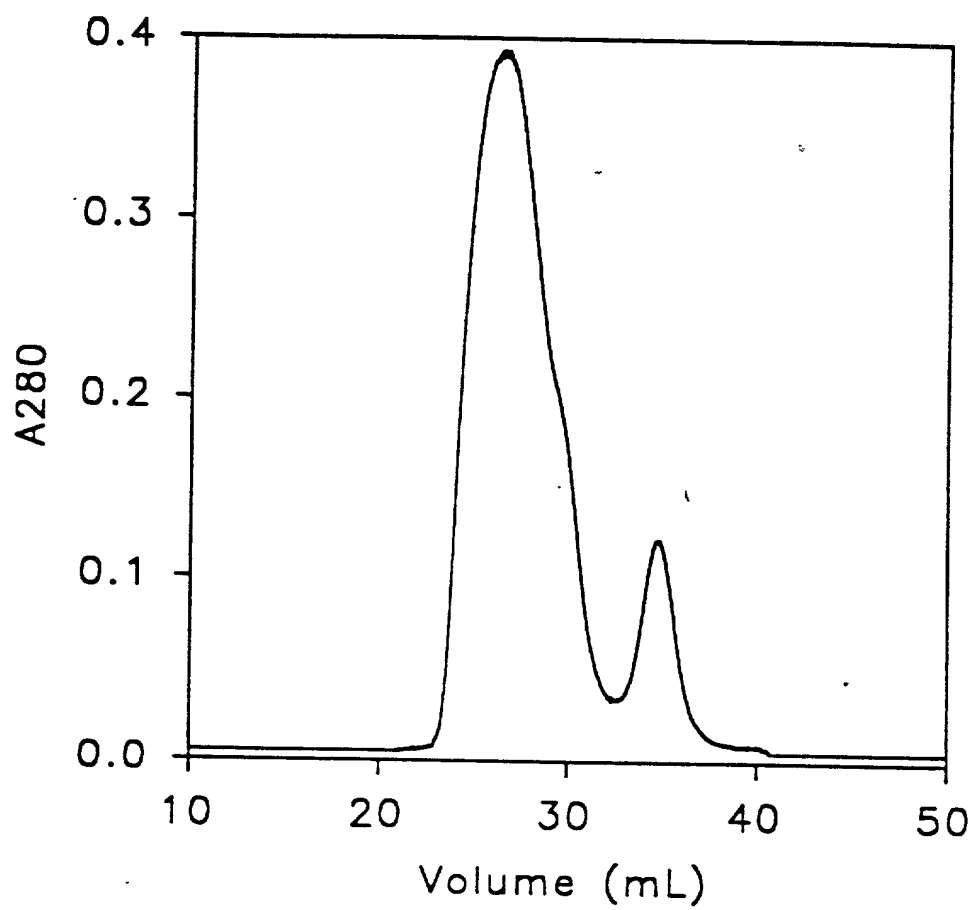


FIG. 40B

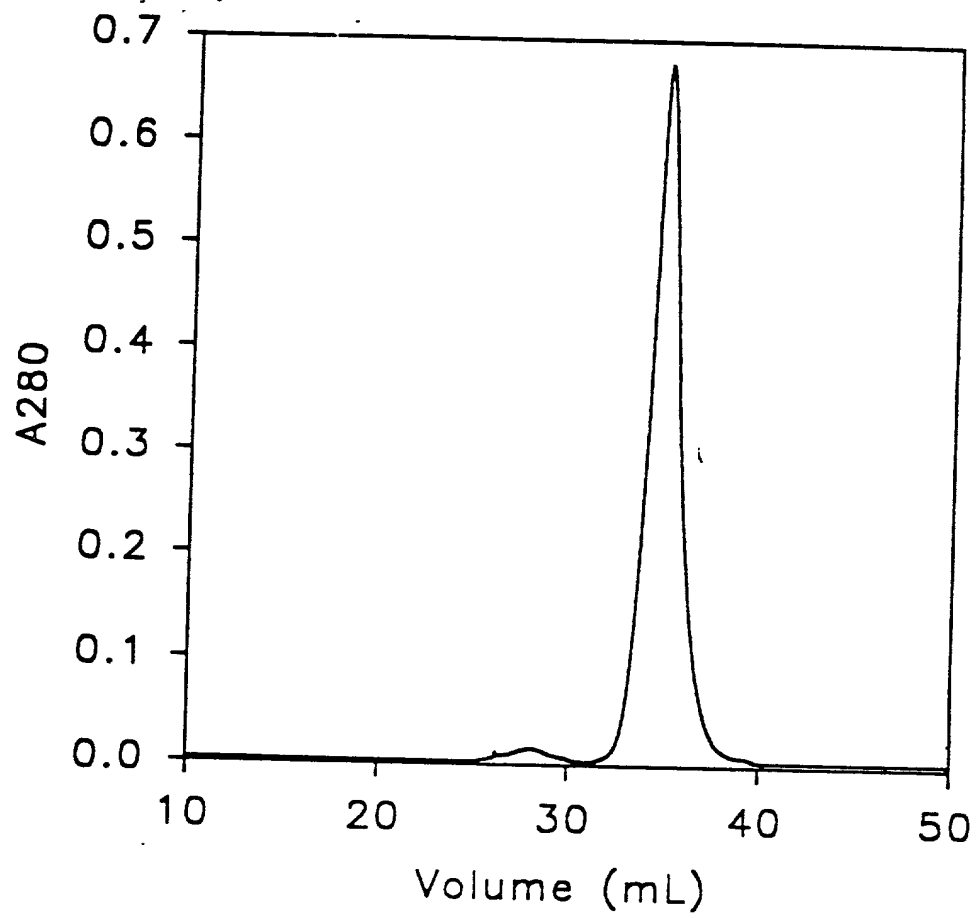


FIG. 41

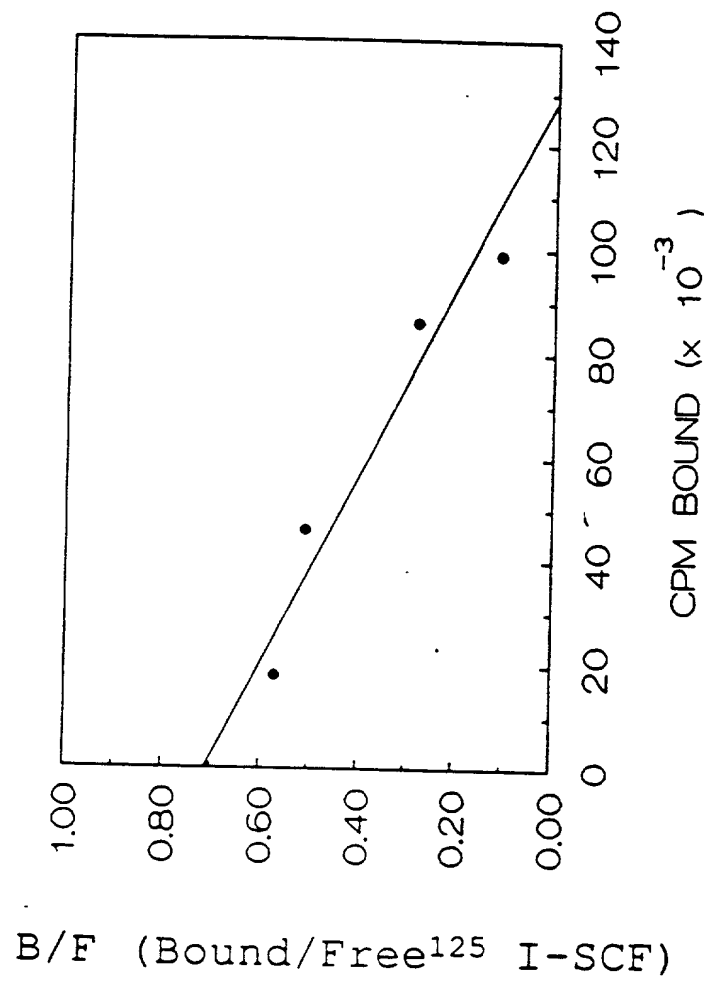


FIG. 42A

CCGCCTCGCGCGGAGACTAGAAAGCGCTGCGGGAAGCAGGACAGTGGAGAGGGCGCTGCGC 61

TCGGGGCTACCCAATGCGTGGACTATCTGCCCGCGCTGTTCGTGCAATATGCTGGAGCTCCA 122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCTTCCTT 183

-25 -20

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228

-10 1

Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG 273

10

Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 318

20

30

Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 363

40

Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 408

50

60

Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT 453

FIG. 42B

Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val	70	80
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG		498
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	90	
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT		543
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe	100	110
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT		588
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala	120	633
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC		
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val	130	140
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT		678
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr	150	
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA		723

FIG.42C

Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn	170
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT	768
Asp Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp	180
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC	813
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser	200
TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT	858
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg	210
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA	903
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu	230
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA	948
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe	240
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT	993
Gln Glu Val End	248
CAA GAA GTG TAA	
TTGTGGCTTGTATCAACACTGTTACTTTTCGTACATTGGC	1044

FIG. 42D

TGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104
 TGGAGTGACAGACCCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164
 AGAAATTGGAACAGAAATGTTTTACTGTGAAACTGGCAGCTGAATTAATCATCTATAAAGAA 1224
 GAACTTGCCATGGAGCAGGACTCTATTTTAAGGACTGCGGGGACTTGGGTCTCATTTAGAAC 1284
 TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTGGCATGGC 1344
 TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

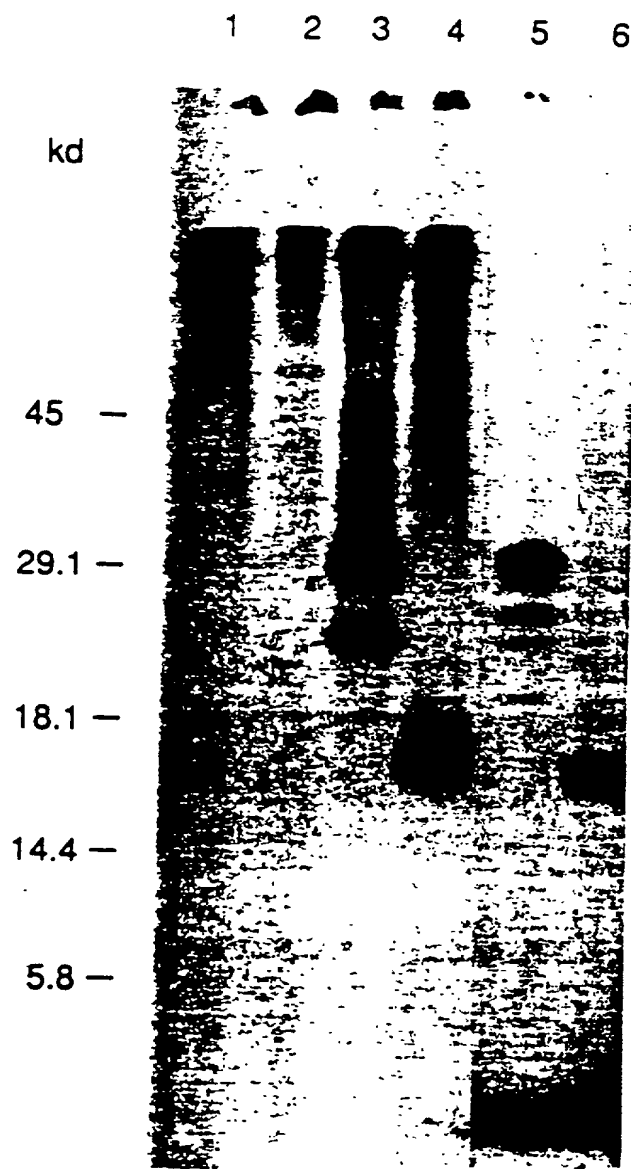


FIG. 44B

Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn	60
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT	420
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val	80
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG	465
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	90
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	510
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe	110
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT	555
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala	120
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC	600
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val	140
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT	645
Ser Ser Thr Leu Ser Pro Glu Lys Gly Lys Ala Lys Asn Pro Pro	150
TCT TCA ACA TTA AGT CCT GAG AAA GGG AAG GCC AAA AAT CCC CCT	690

FIG. 44C

160 Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu 170
 GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG 735

 Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
 TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG 780

 190 Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile 200
 AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT 825

 210 Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg 870
 AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA

 220 Glu Phe Gln Glu Val End
 GAG TTT CAA GAA GTG TAA TTGTGGCTTGTATCAACACTGTTACTTTCGTA 920
 CATGGCTGGTAAACAGTTTCATGTTTGTCTTCATAAATGAAGCAGCCTTTAAACAATTCATA 980
 TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG 1040
 ATGATTCAGAAATTGGAACAGAAATGTTTACTGTGAAACTGGCACTGA 1088

FIG. 45

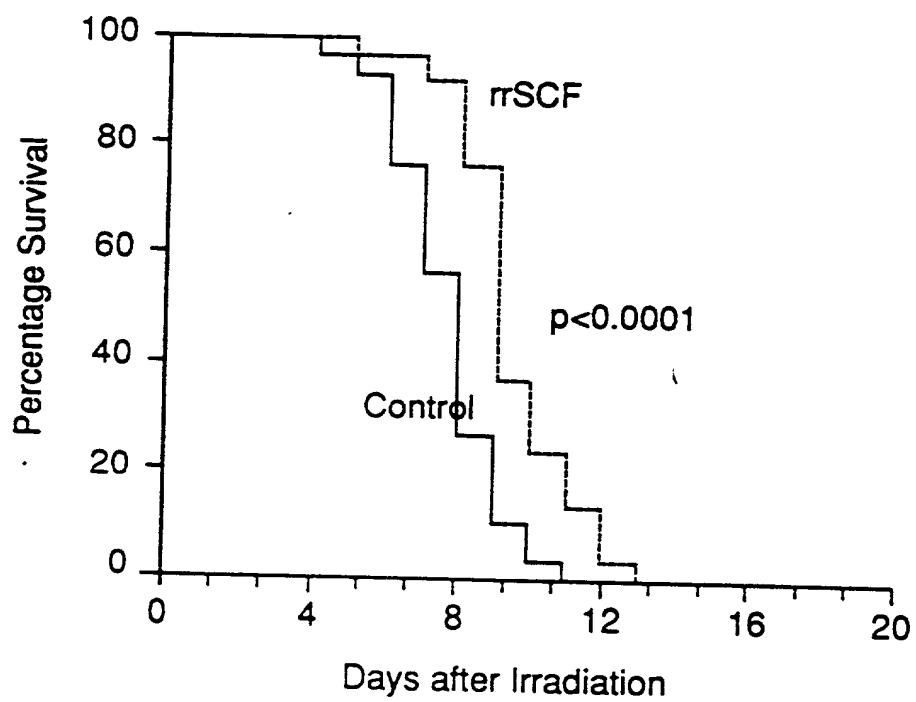
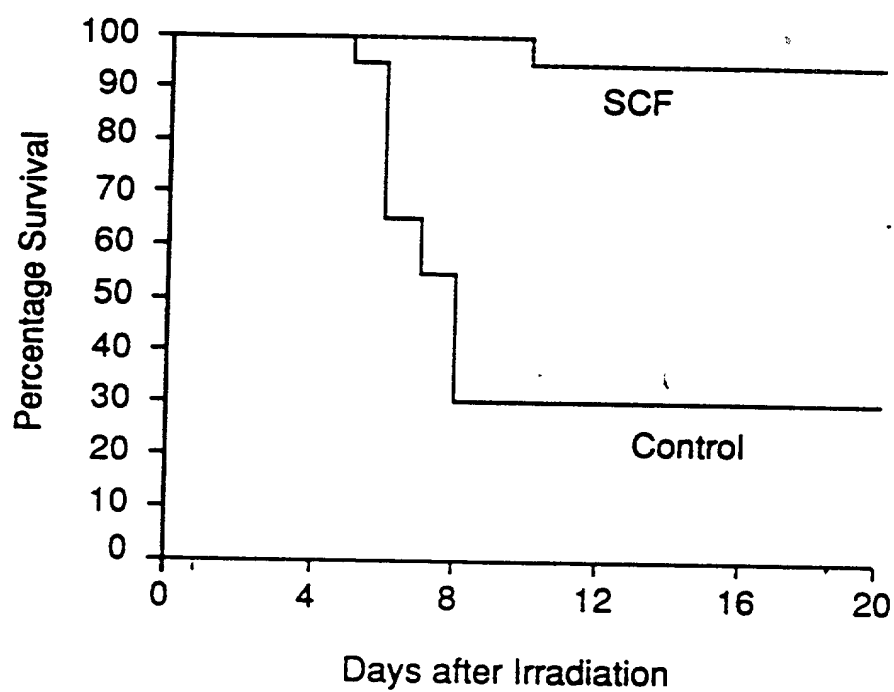
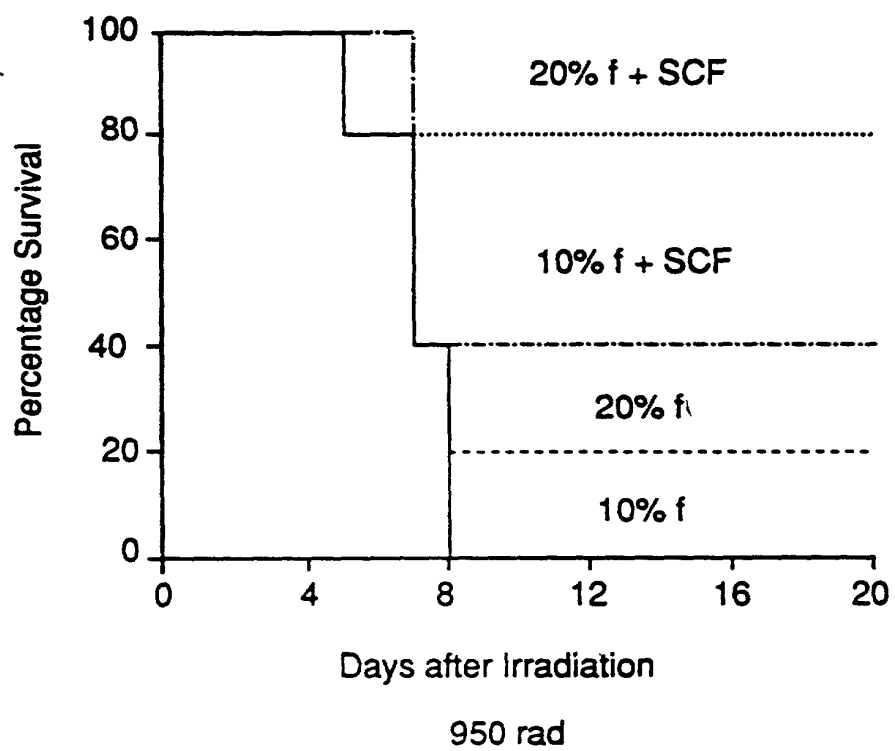


FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47



[illegible]

SCF RADIOPROTECTION (1163 RAD)

Normal Female BDF1 mice, n=30

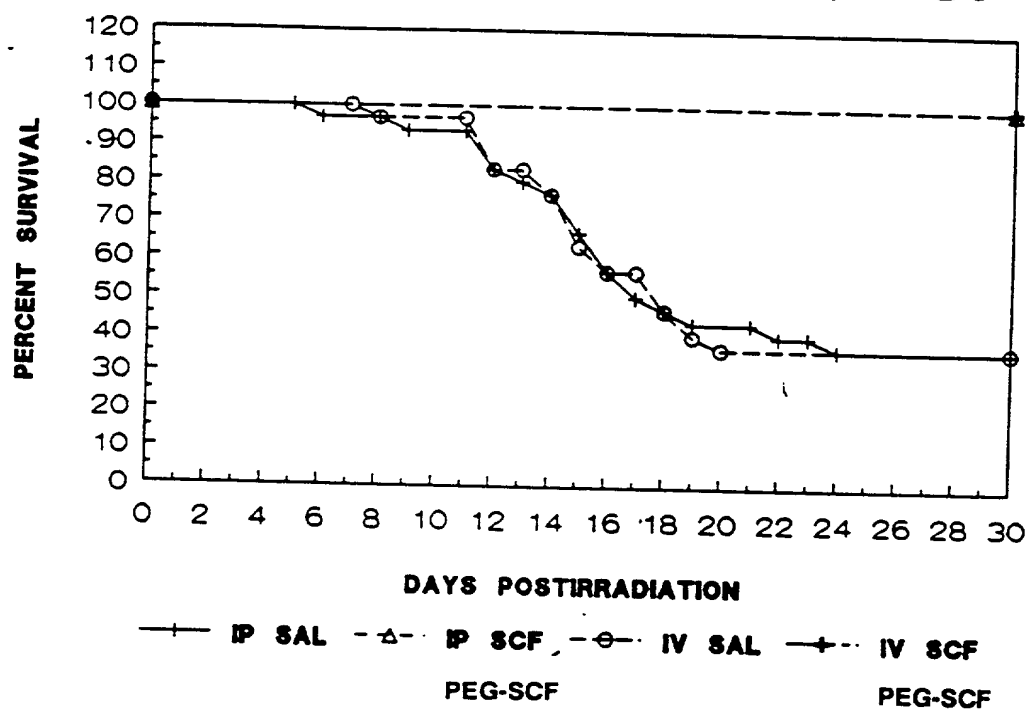


FIG. 49

SCF RADIOPROTECTION (1159 RAD)

Normal Female BDF1 mice

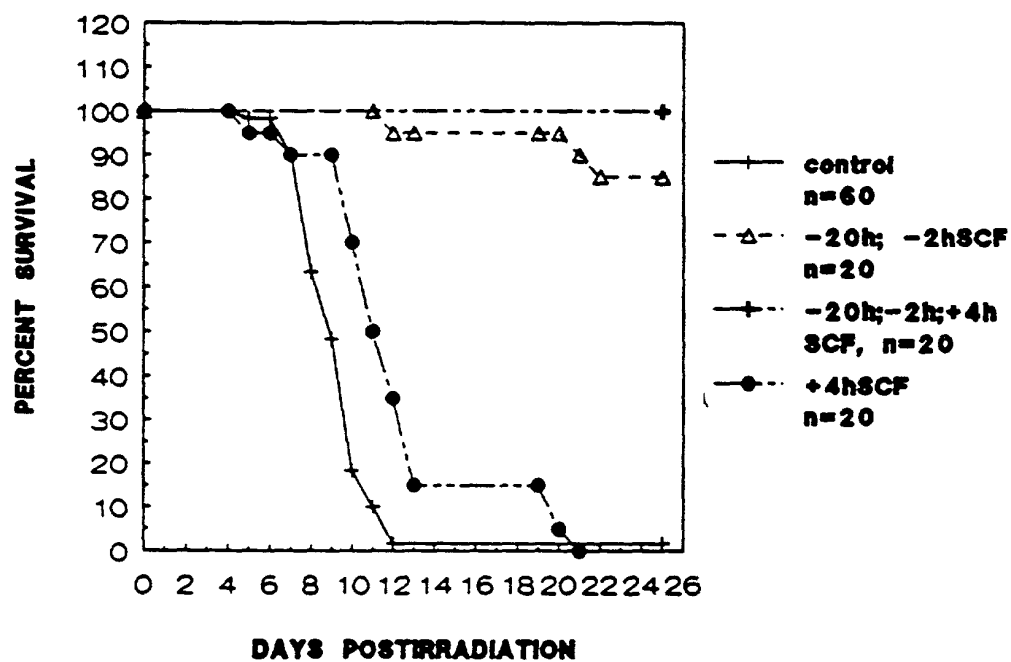


FIG. 50

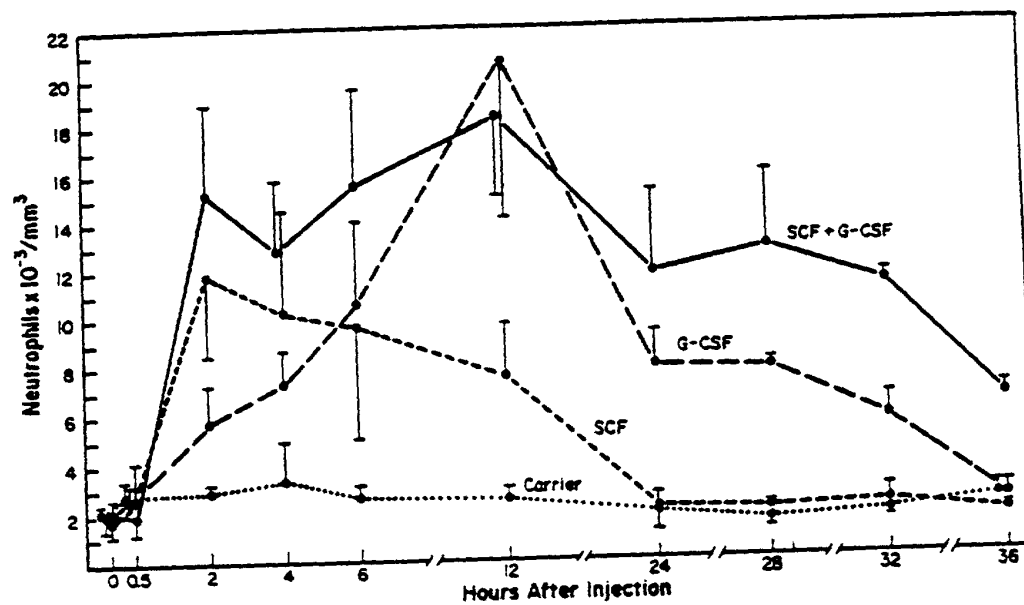


FIG. 51

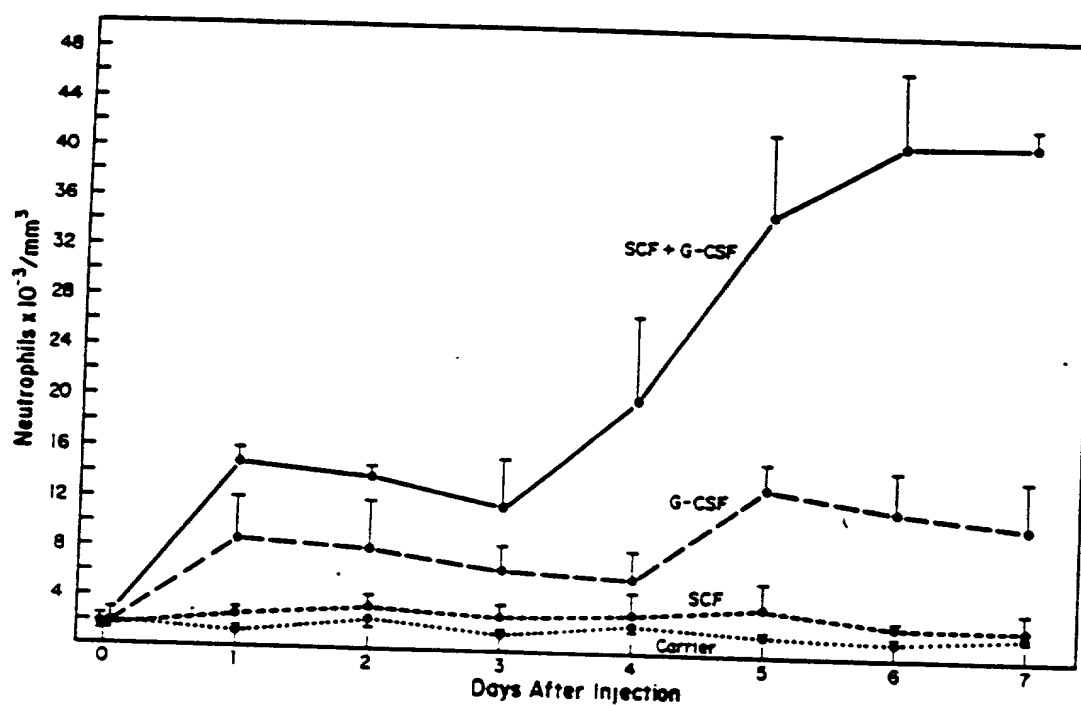


FIG. 52

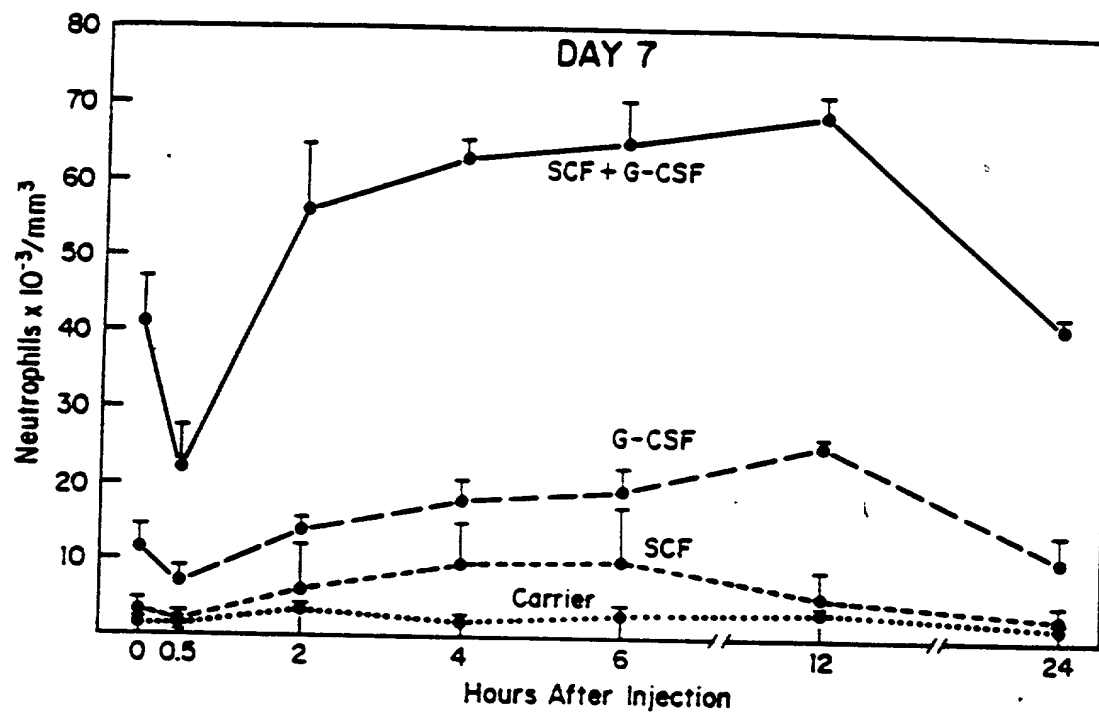


FIG. 53

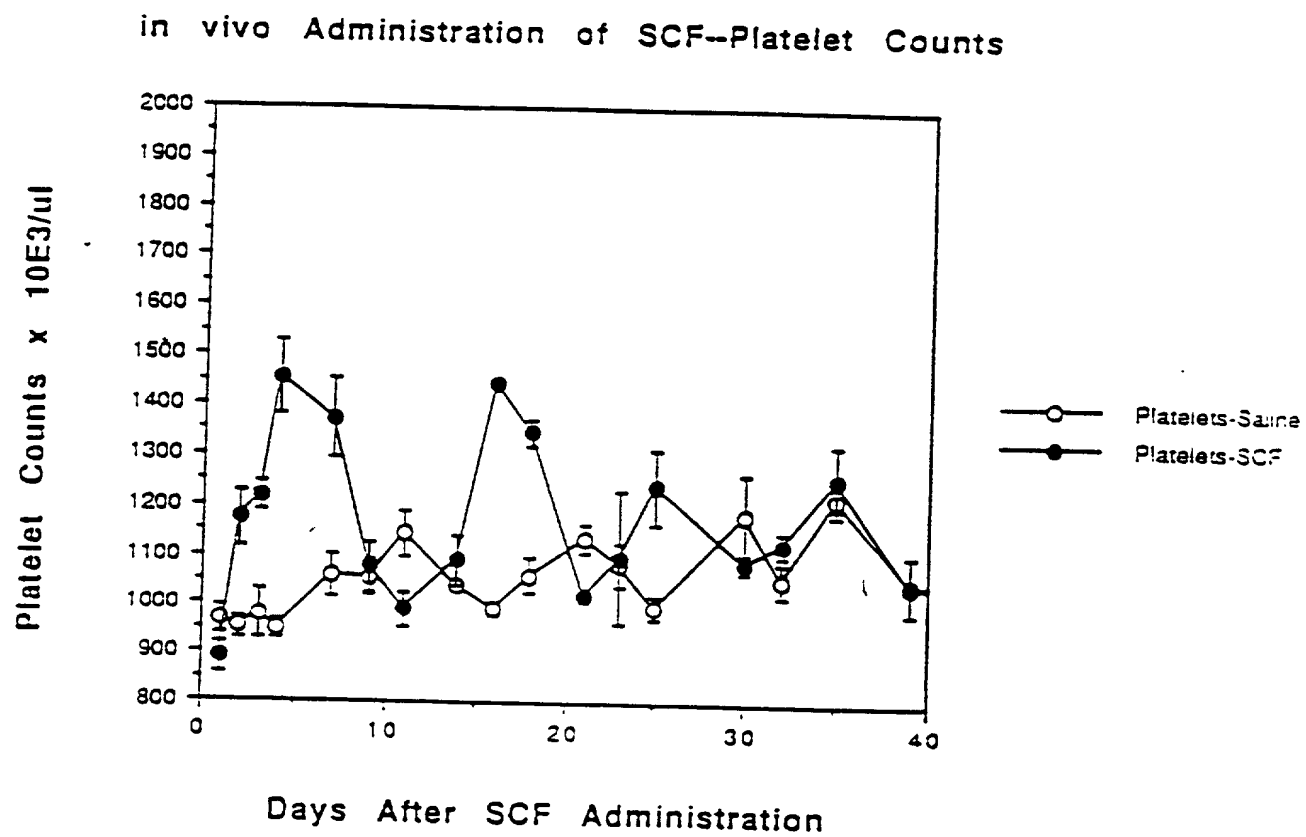


FIG. 54

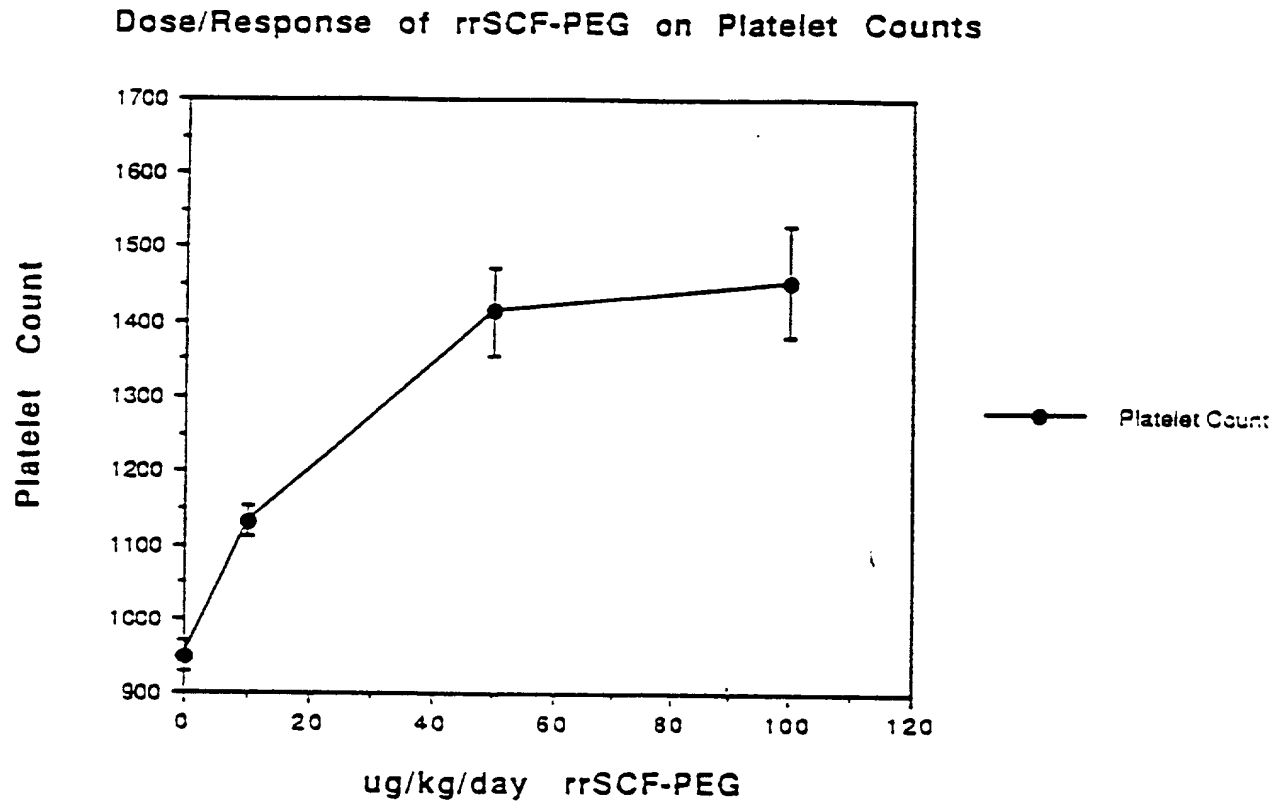


FIG. 55

Effect of 5-FU on platelet levels

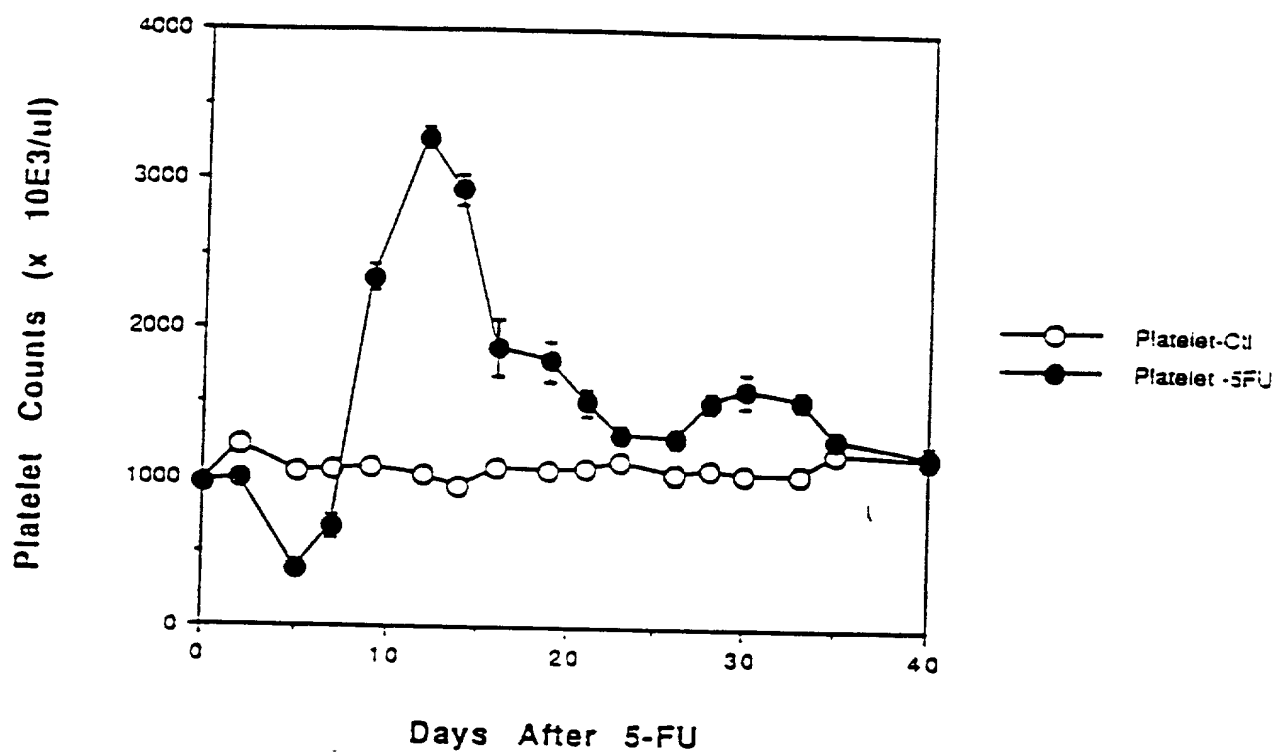
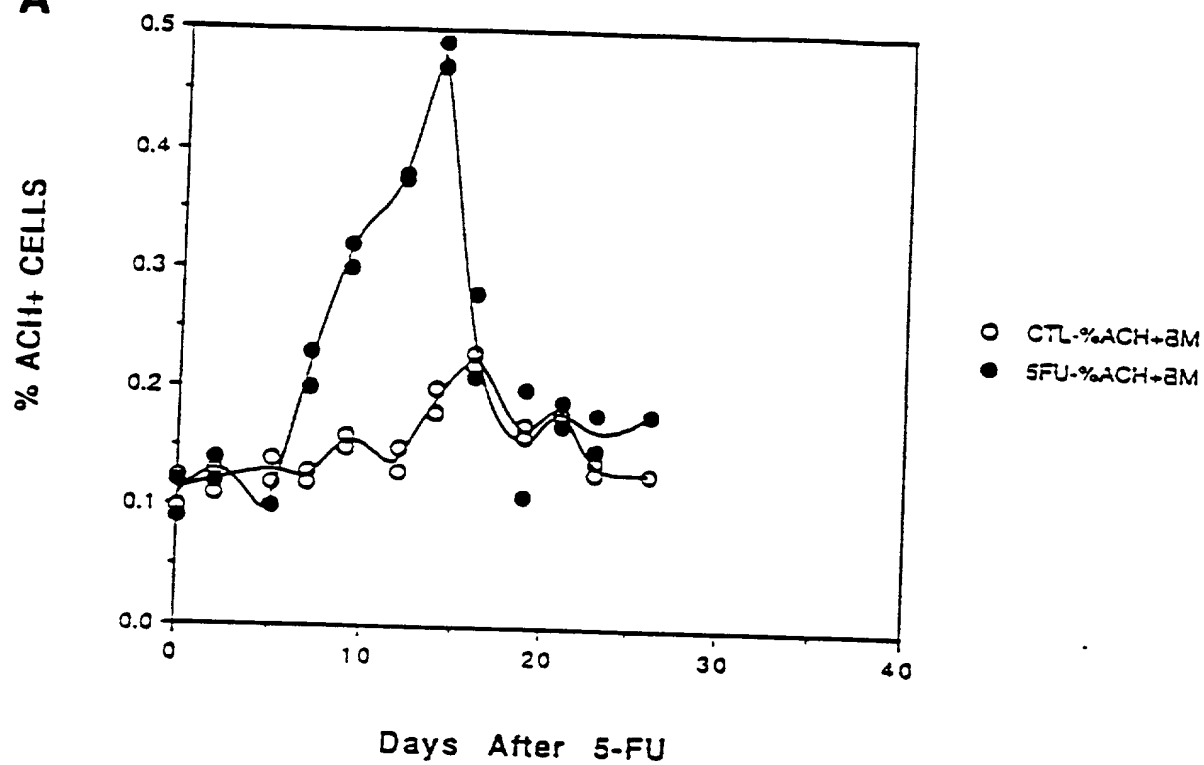


FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

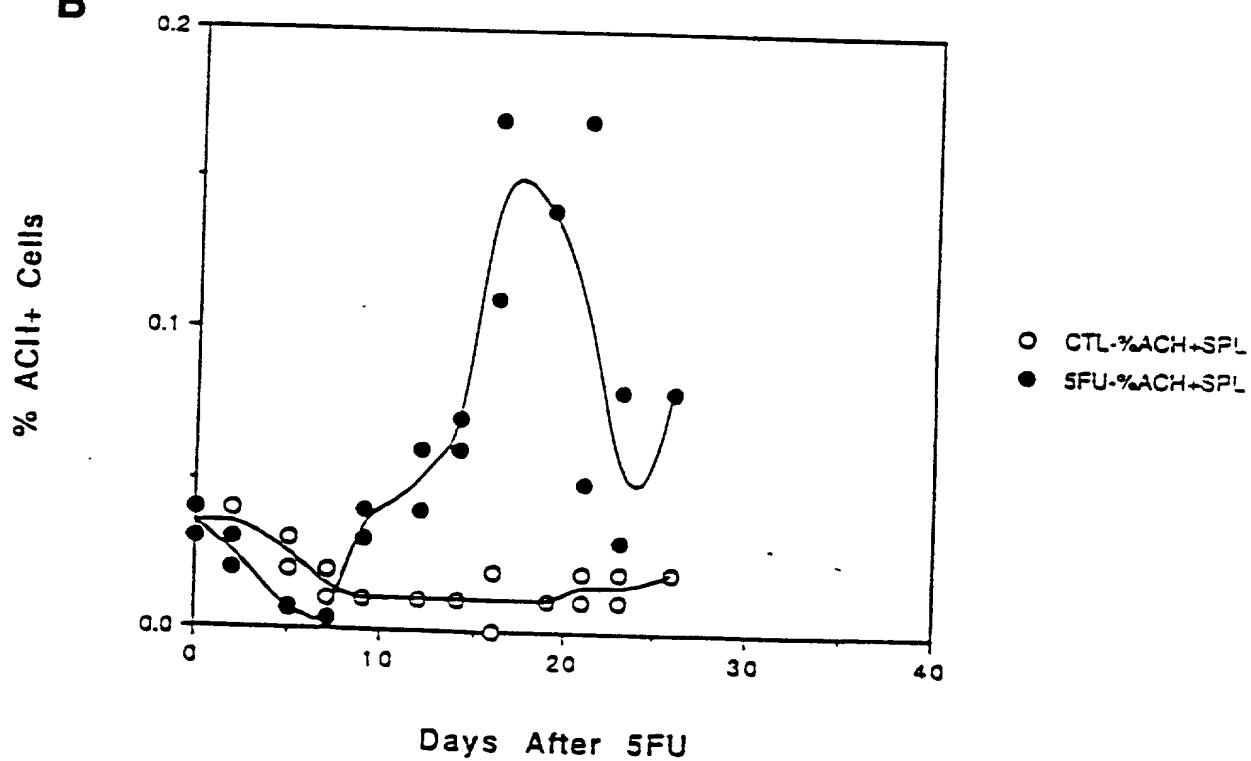


FIG. 57

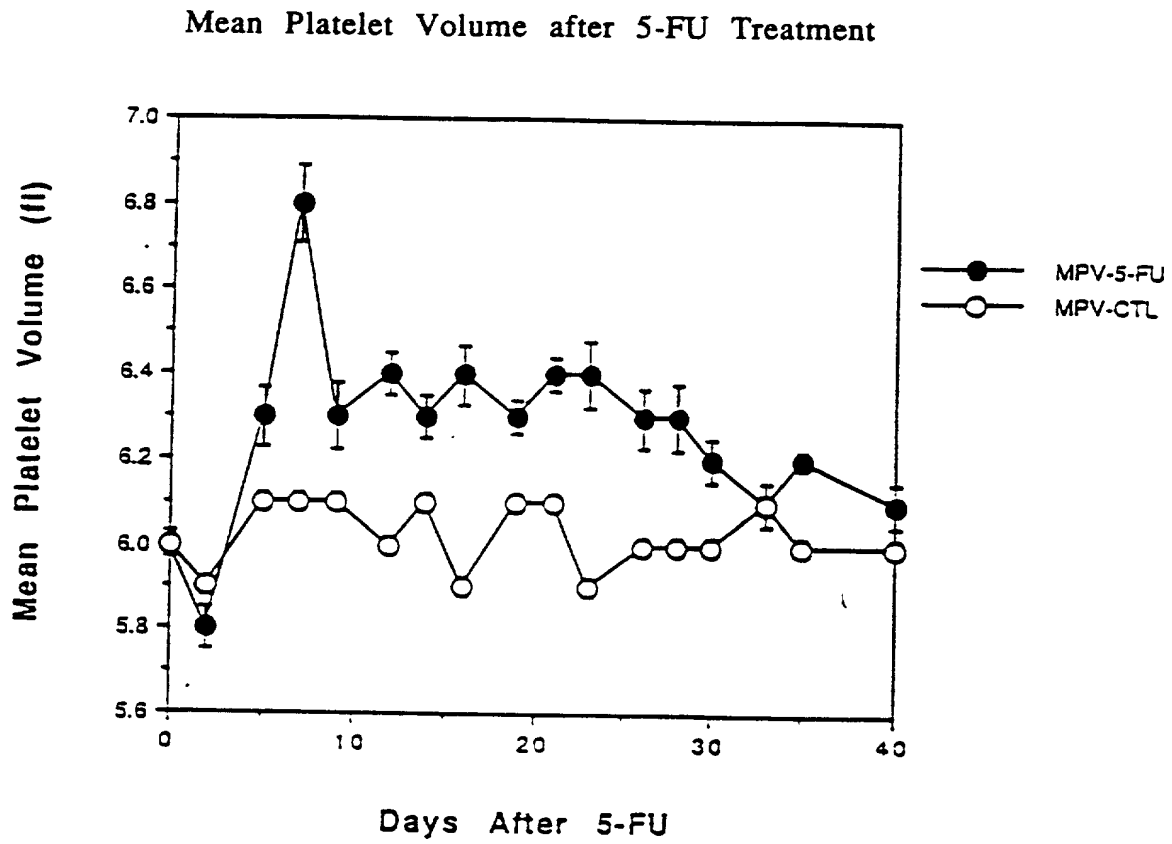


FIG. 58

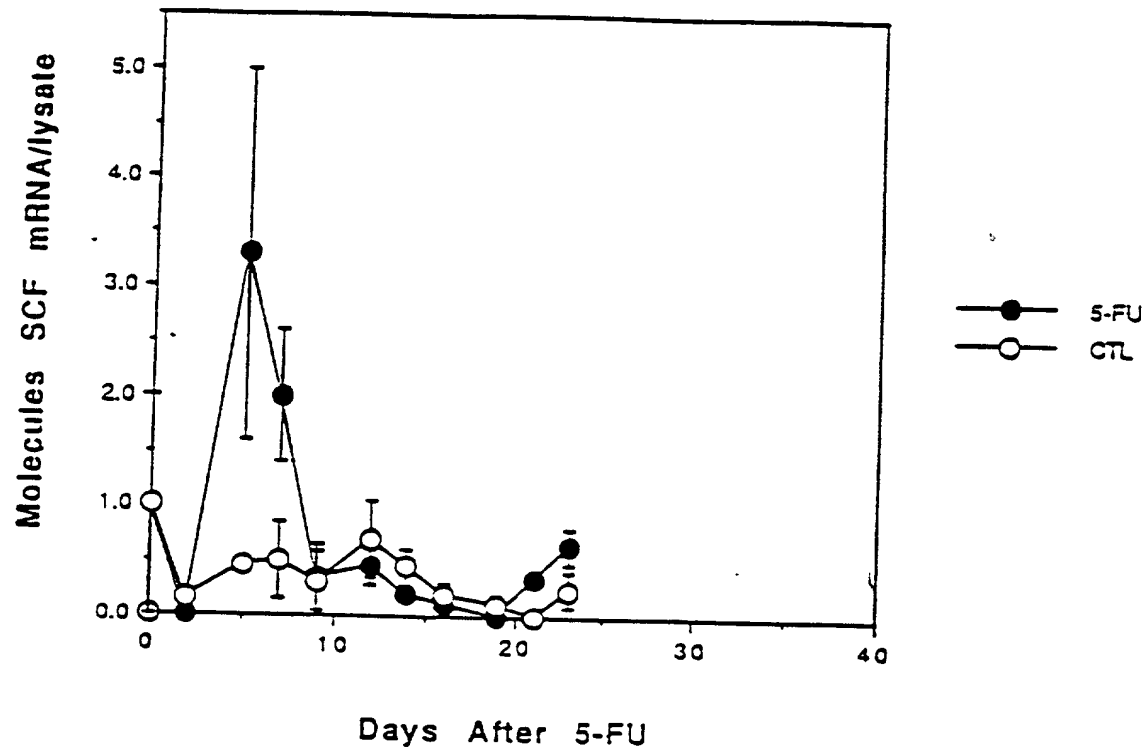


FIG. 59

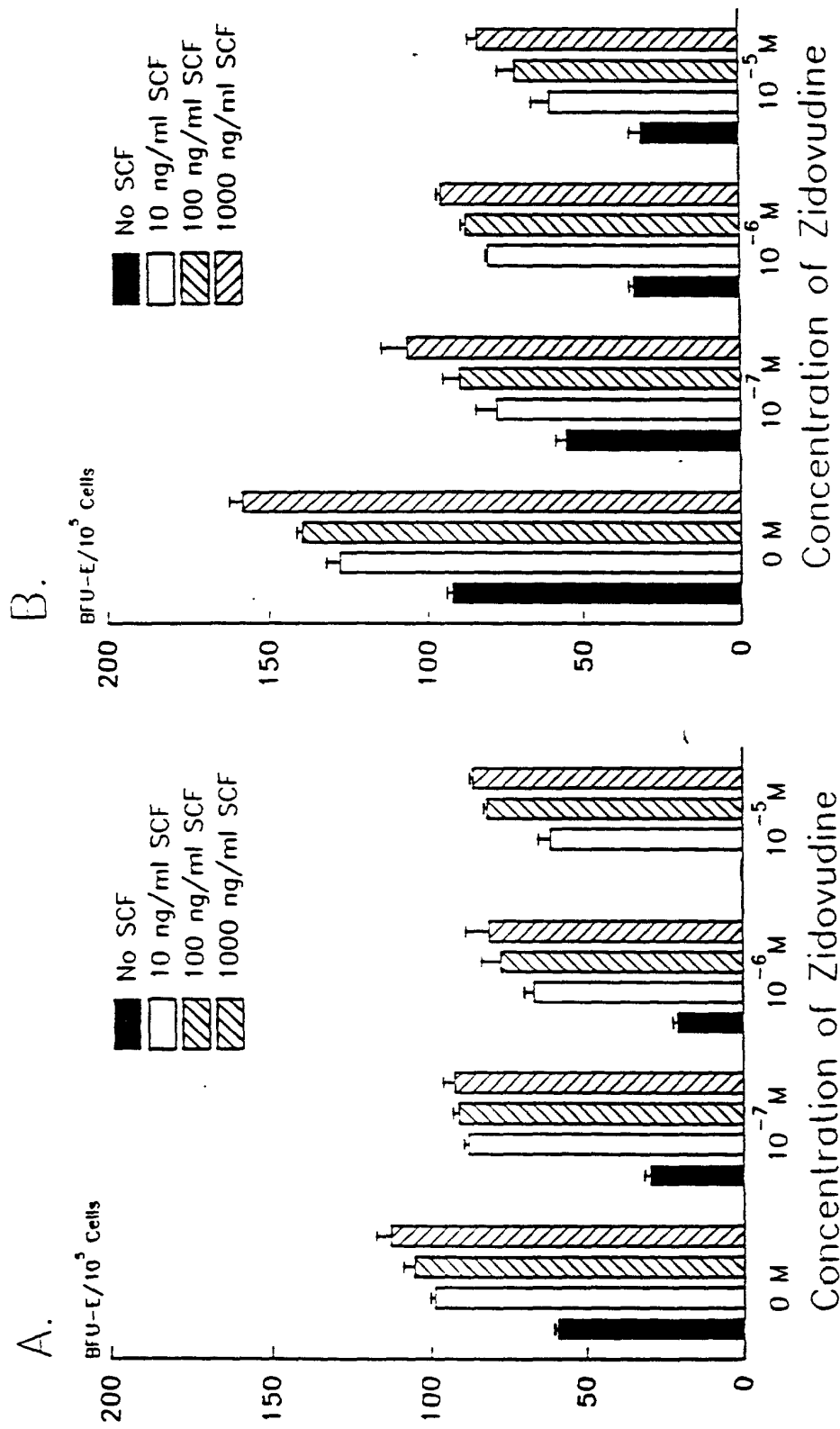


FIG. 60

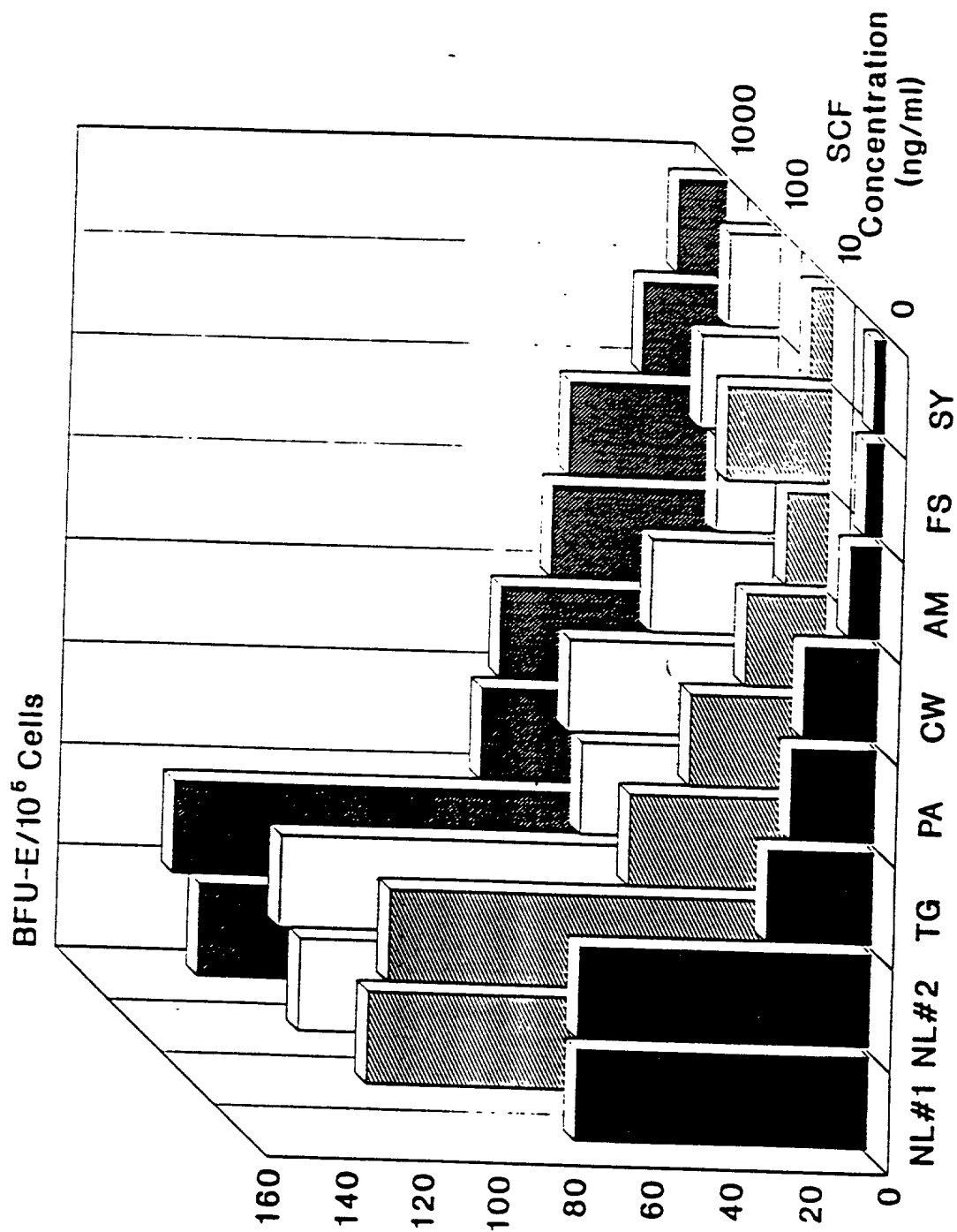
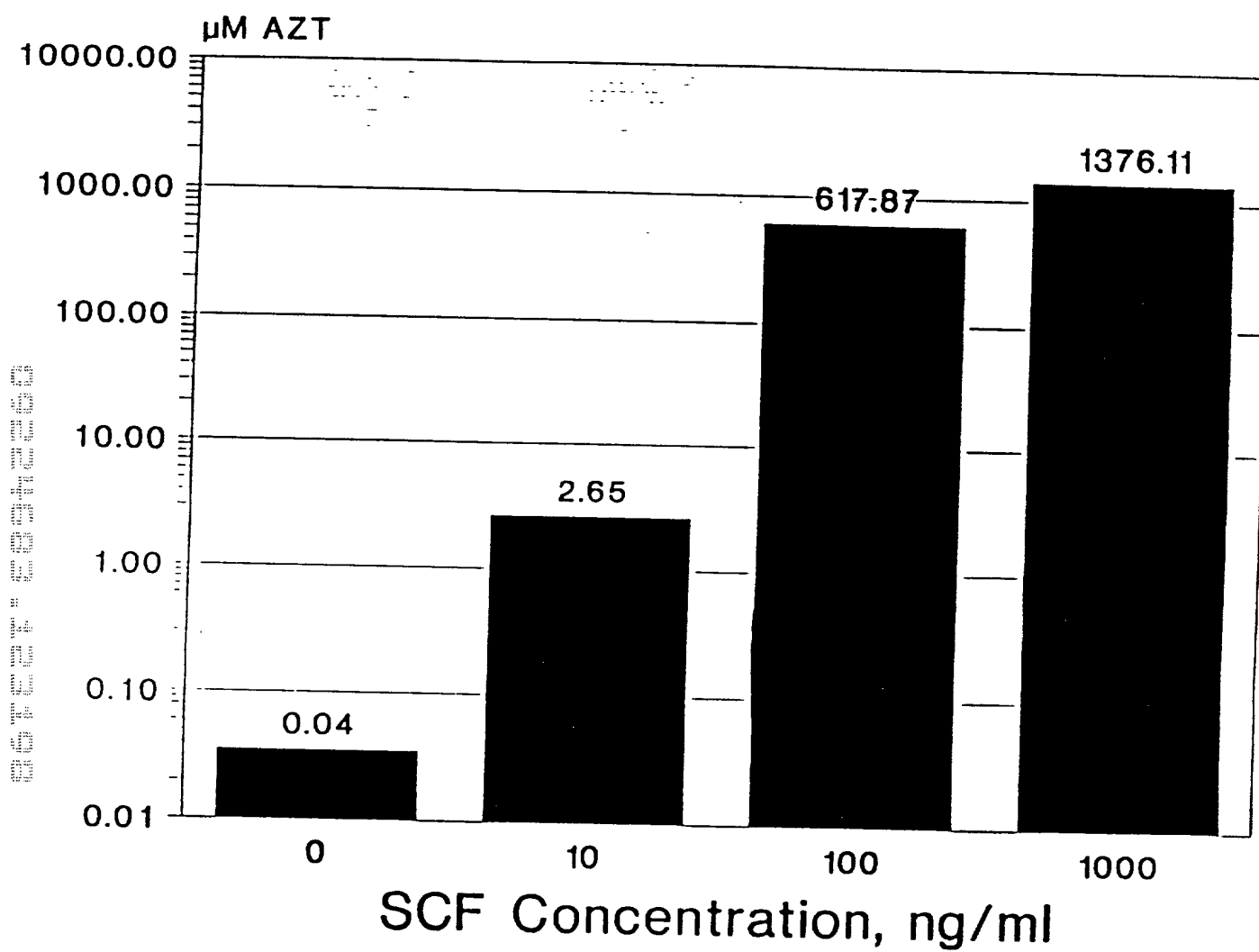
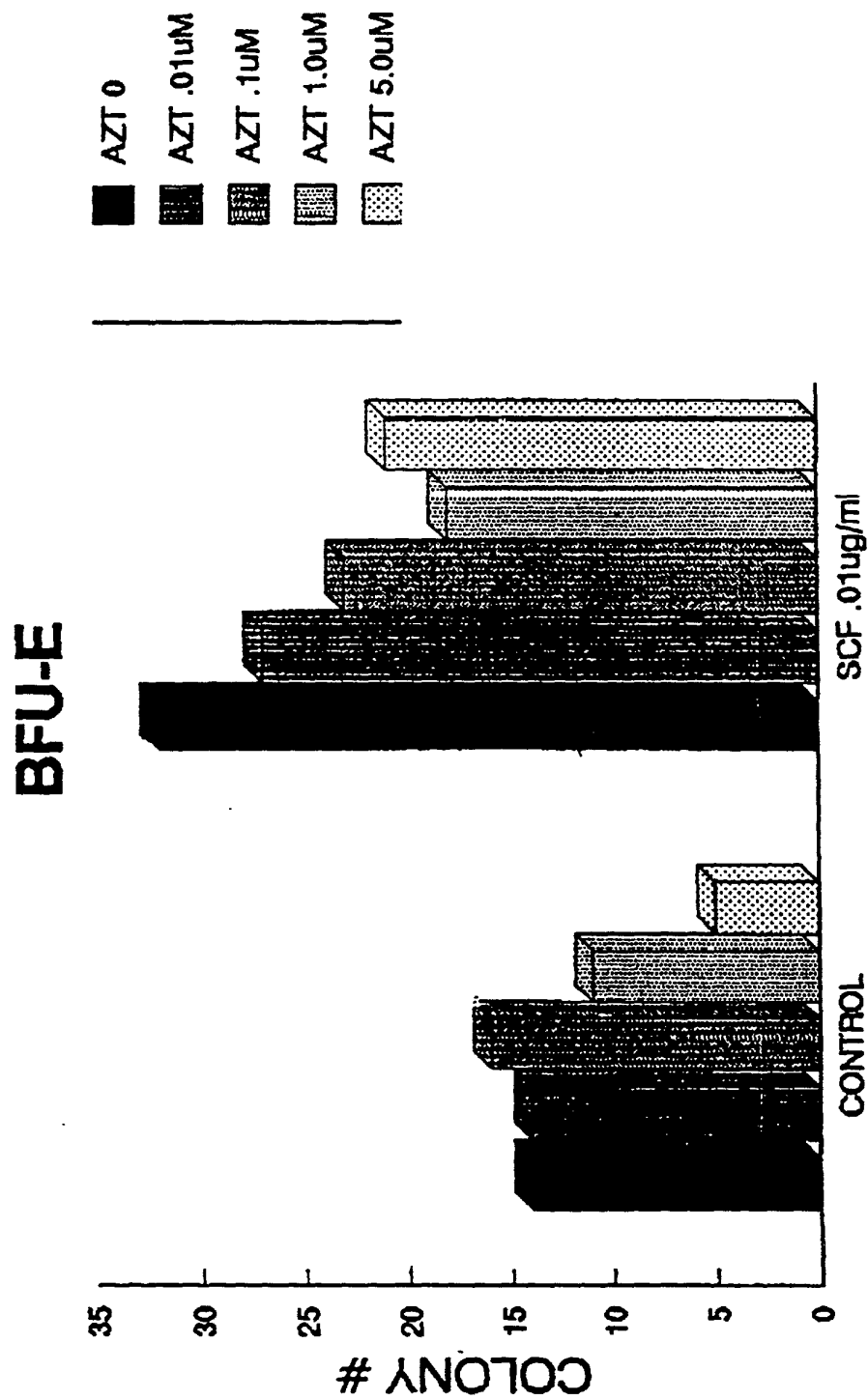


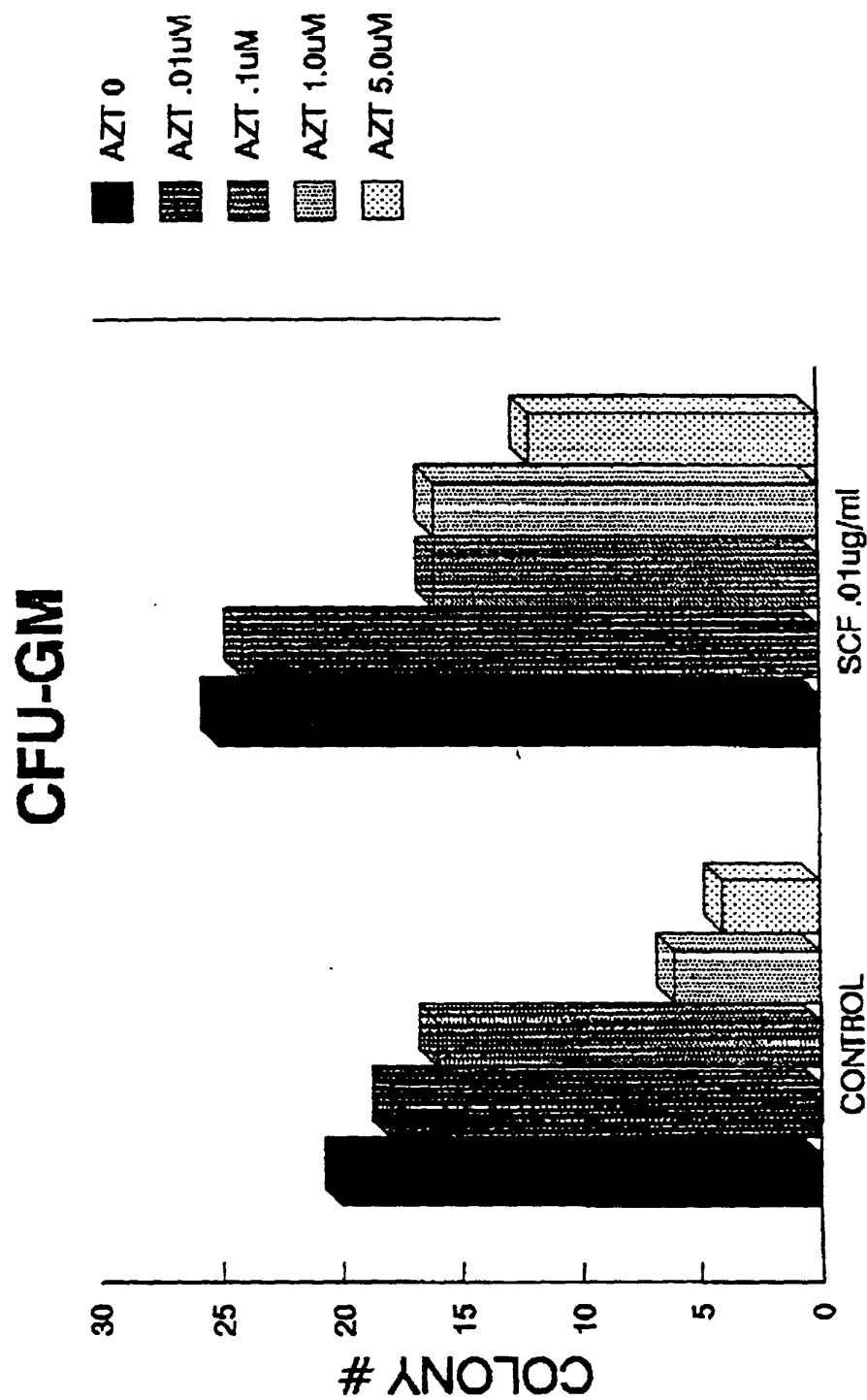
FIG: 61



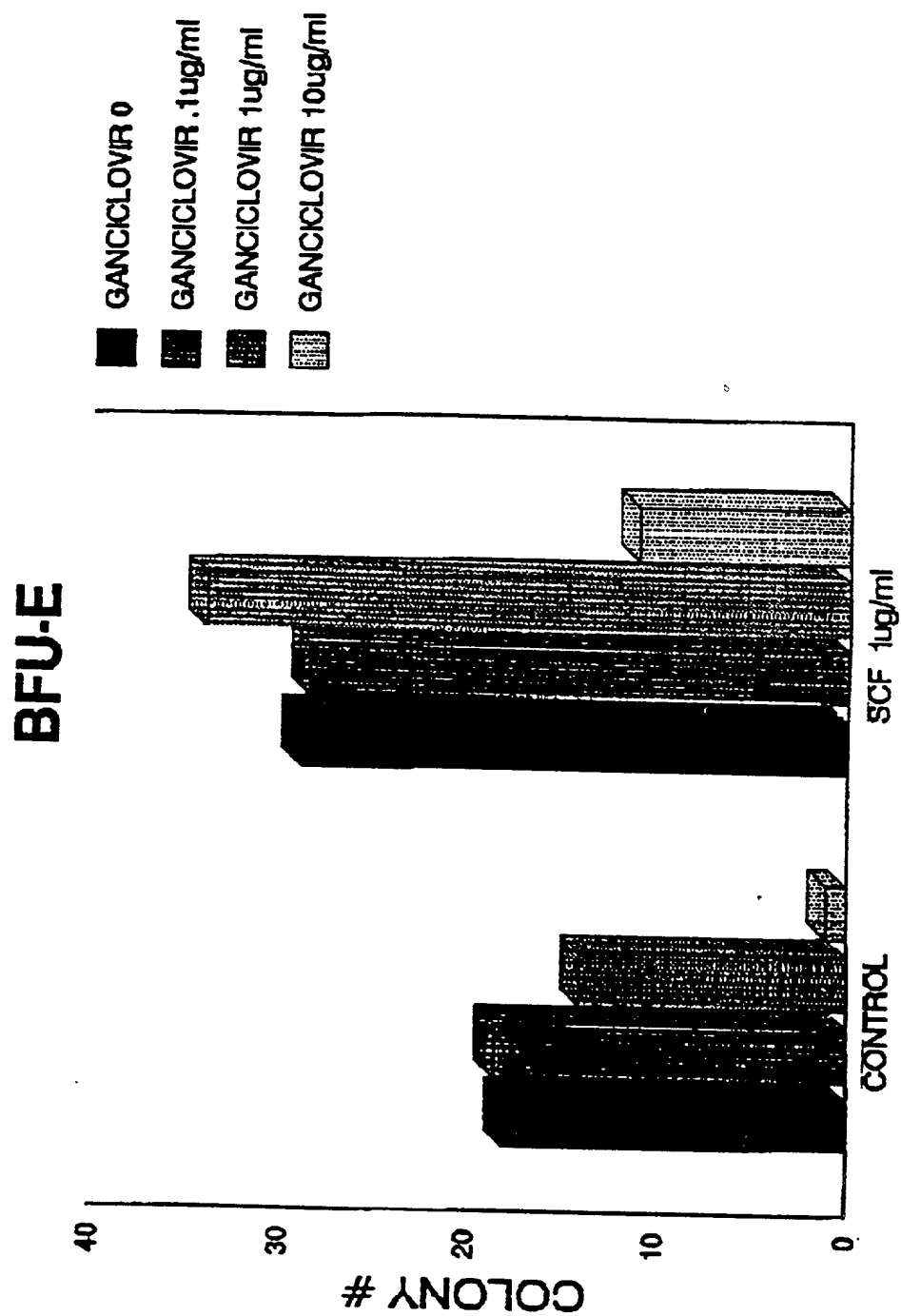
EFFECT OF SCF ON AZT SUPPRESSION OF BMC



EFFECT OF SCF ON AZT SUPPRESSION OF BMC



EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC



EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

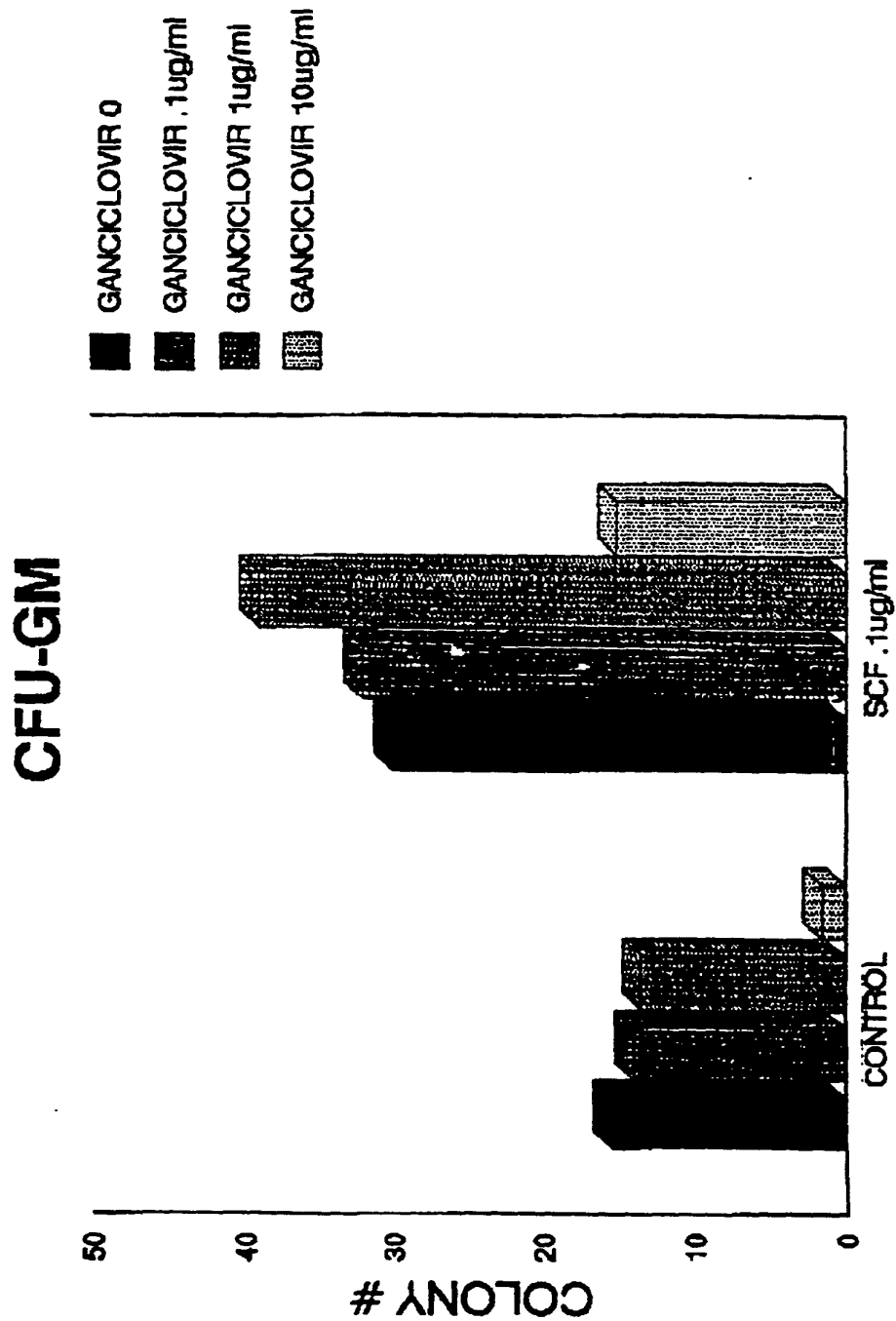


FIG. 66

Effects of SCF on CFU-S Number

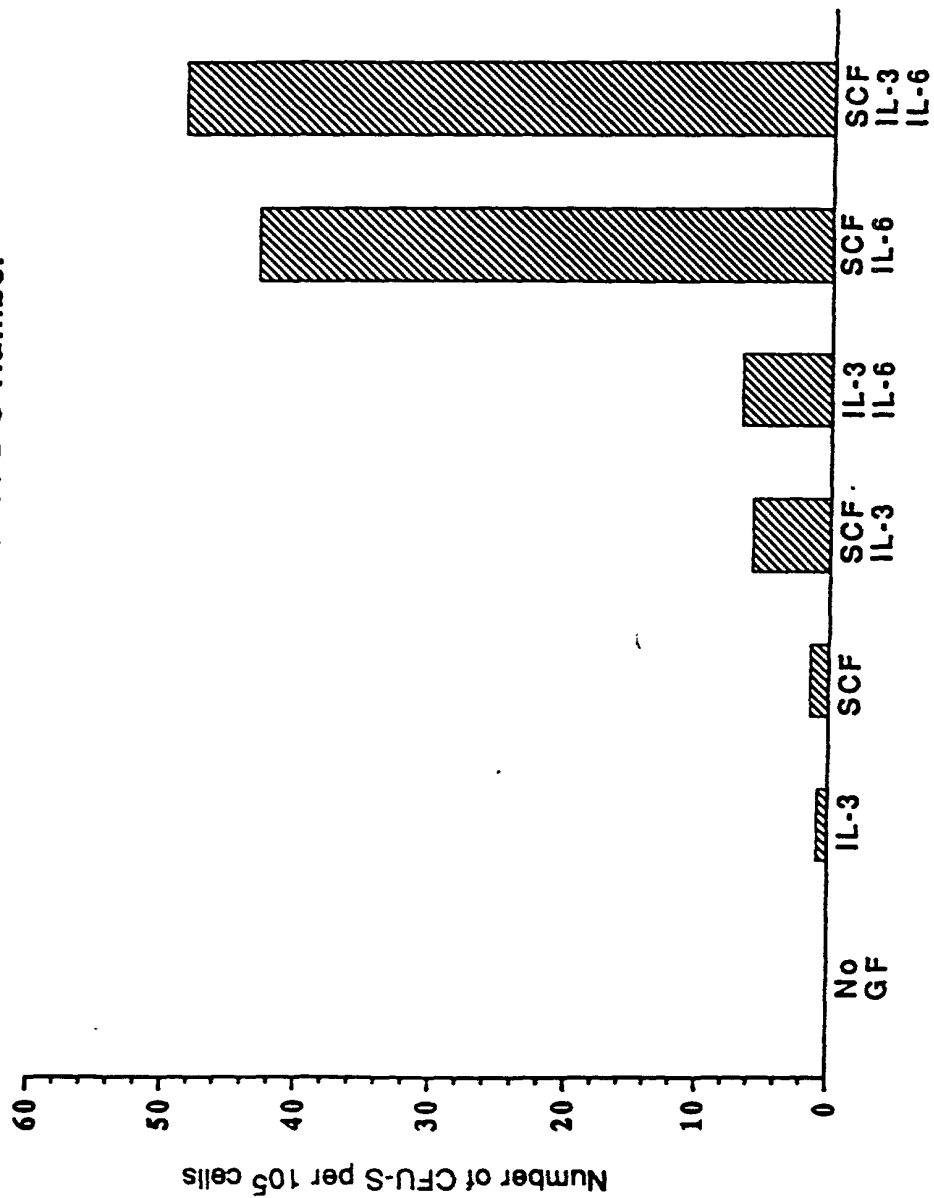
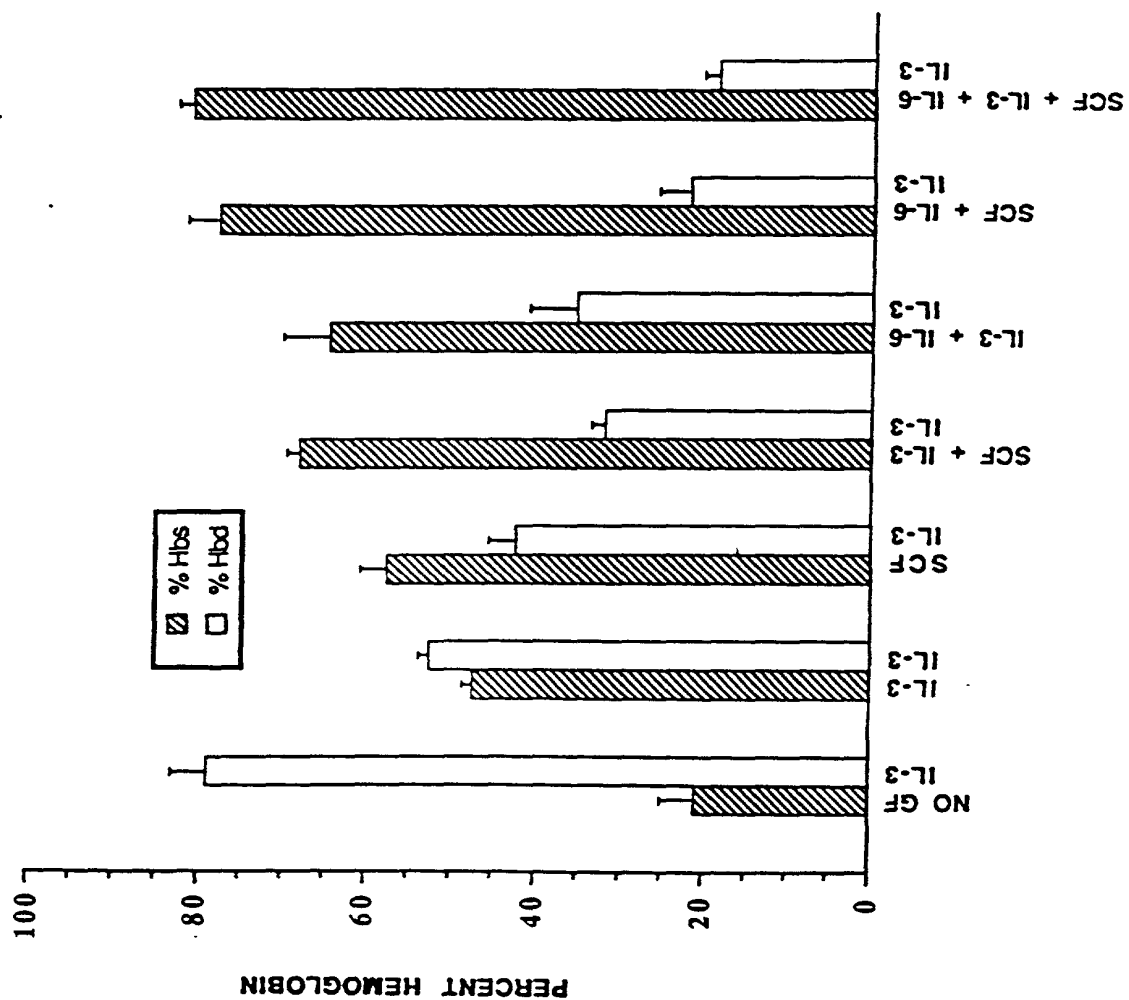
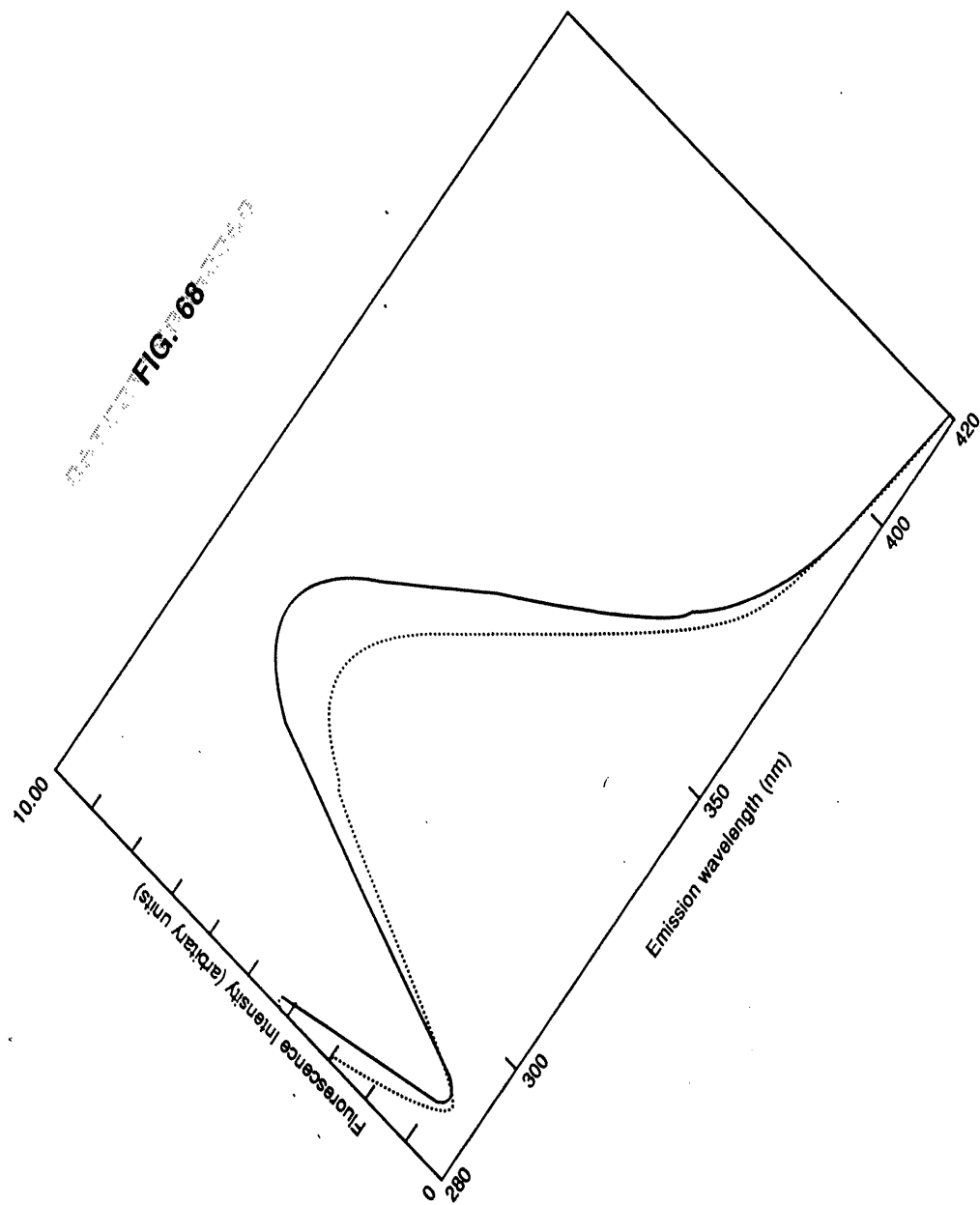


FIG. 67

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)





Sheet 1 FIG. 69A 60

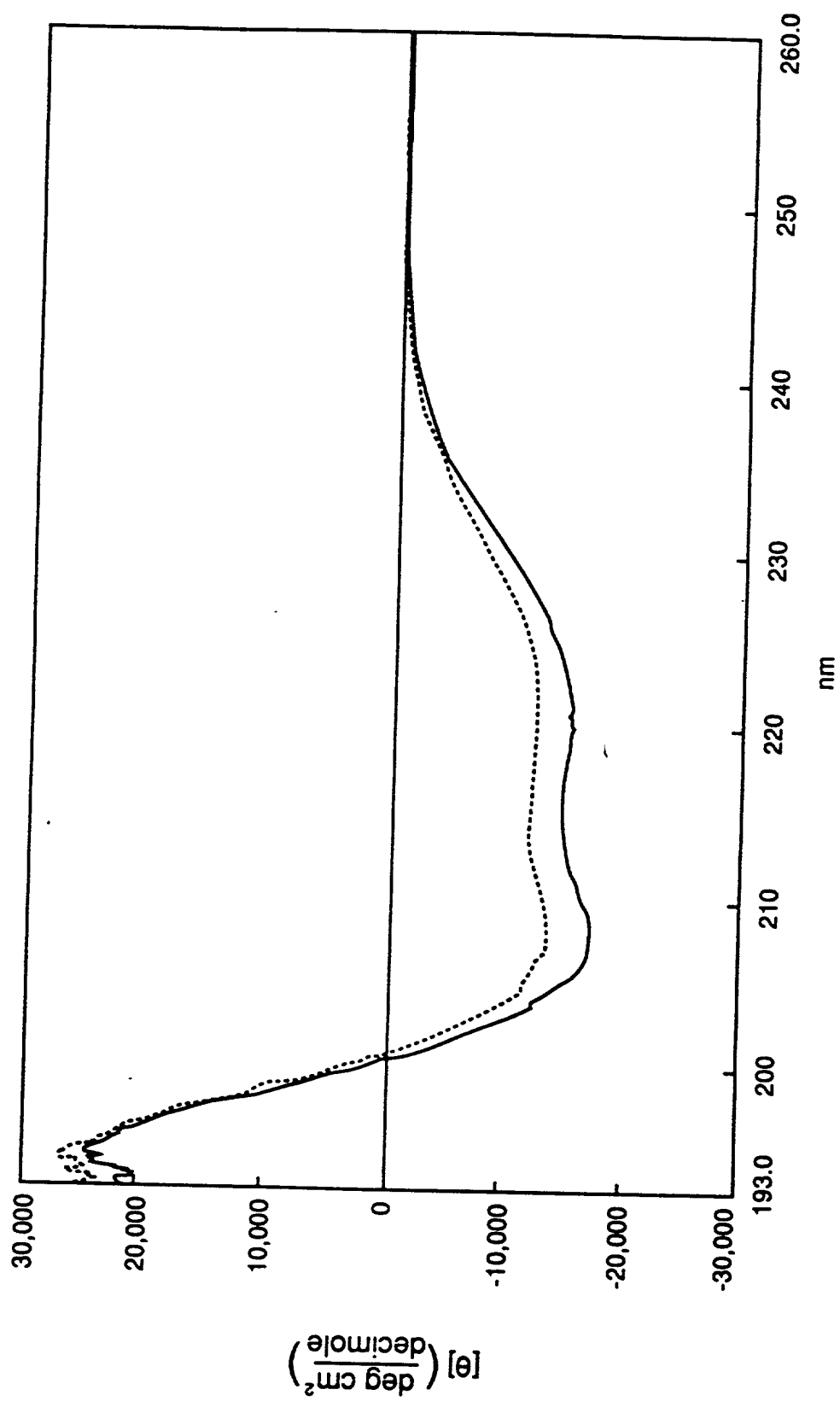


FIG. 69B

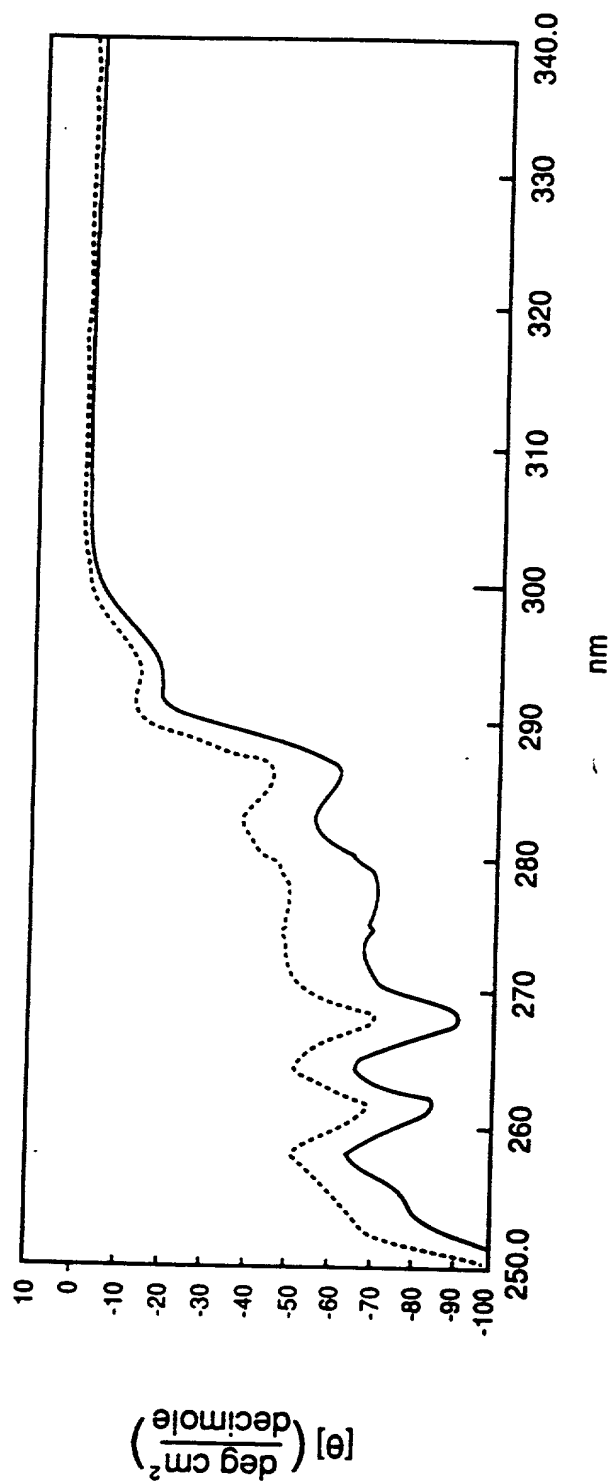


FIG. 70

